

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:01 ; Search time 30.701 Seconds  
(without alignments)  
2504.793 Million cell updates/sec

Title: US-09-811-131-32  
Perfect score: 1547  
Sequence: 1 MTDALSPAKDFLAGVAA.....LRMGAPVLVLYDEIKYT 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP virus:\*  
16: SP bacteriophage:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1515	97.9	298	6	Q8S0H5
2	1450	93.7	298	11	Q8JH10
3	1446	93.5	298	13	Q8PH11
4	1443	93.3	298	13	Q8PH12
5	1443	93.3	298	13	Q8PH13
6	1439	93.0	298	13	Q8PH14
7	1425	92.1	298	13	Q8PH15
8	1423	92.0	298	6	Q8S0H5
9	1417	91.6	298	11	Q8JH10
10	1295	83.7	317	13	Q8PH11
11	1278	82.6	299	5	Q8S0H5
12	1253.5	81.0	312	5	Q8S0H5
13	1248.5	80.7	300	5	Q8S0H5
14	1190.5	77.0	288	5	Q8S0H5
15	1185.5	76.6	288	5	Q8S0H5
16	1146	74.1	254	11	Q8PH11

17	1145.5	74.0	304	5	Q25129
18	1125.5	72.8	307	5	Q62526
19	1102	71.2	315	4	Q9H0C2
20	1040.5	67.3	310	10	Q8H727
21	1032	66.7	300	5	Q45865
22	1029	66.5	313	5	Q21103
23	1029	66.5	313	5	P91410
24	986	63.7	300	5	Q01813
25	985	63.7	309	5	Q97470
26	983	63.5	300	5	Q17407
27	950.5	61.4	318	5	Q9B3J6
28	949.5	61.4	307	8	Q9XM22
29	942	60.9	301	5	Q8J1J4
30	939	60.7	301	5	Q25692
31	938	60.6	301	5	Q26006
32	932	60.2	301	5	Q8MVR4
33	929	60.1	305	5	Q8MVR7
34	925	59.8	308	5	Q8MVR8
35	919	59.4	306	5	Q8MVR5
36	915	59.1	308	5	Q8MVR6
37	819	52.9	170	6	Q9X859
38	778	50.3	305	3	Q9P8M1
39	764.5	49.4	302	3	Q8J0M2
40	759	49.1	326	5	P91270
41	755	48.8	303	3	Q74260
42	753	48.7	317	5	Q9N647
43	752	48.6	307	5	Q76286
44	750	48.5	386	10	P93767
45	749.5	48.4	306	5	Q18683

## ALIGNMENTS

### RESULT 1

ID	Q8S0H5	PRELIMINARY	PRT	298 AA.
AC	Q8S0H5			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Adenine nucleotide translocator 2.			
OS	Bos taurus (Bovine)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yamazaki N., Shinohara Y., Tanida K., Terada H.;			
RT	"Structural properties of mammalian mitochondrial ADP/ATP carriers:			
RT	RT identification of possible amino acids that determine functional			
RT	differences in its isoforms."			
RL	Mitochondrion 1:371-379 (2002).			
DR	EMBL, AB065433, BAB84673.1;			
DR	InterPro, IPR001993; Mitoch. carrier.			
DR	Pfam, PF00153; mito. catr; 3.			
DR	PROSITE, PS00215; MITOCH. CARRIER; 3.			
SQ	SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;			

Query Match	97.9%	Score 1515	DB 6	Length 298
Best Local Similarity	97.7%	Pred. No. 5.2e-126		
Matches 291	Conservative 4	Mismatches 3	Indels 0	Gaps 0
QY	1	MTDALSPAKDFLAGVAAAIISKTAAPVPIERVKLLQVQASRQITPDQKYGIIIDCVVR	60	
DB	1	MTDALSPAKDFLAGVAAAIISKTAAPVPIERVKLLQVQASRQITPDQKYGIIIDCVVR	60	
QY	61	IPKQEVLSFWRGVLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYFAGNLAAG	120	
DB	61	IPKQGVLSFWRGVLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYFAGNLAAG	120	
QY	121	GAAGTSLCFVYPIIDPAPRTLLADVGKAGAEERERGGIDCLVYKXSDGKGLYQGRNVS	180	

Db 121 GAGGATSLCPVYPLDFARTRLAADYKGAAGAEERFRLGCPVYKITYPSDGLRGLYQGFENN 180

QY 181 VGGIIYYRAAAYFGIYDTAKGMLPDPKNTIIVISWMTAQTVTVAAGLTSPYEDTVRRRMM 240

Db 181 VGGIIYYRAAAYFGIYDTAKGMLPDPKNTIIVISWMTAQTVTVAAGLTSPYEDTVRRRMM 240

QY 241 QSGRGKGTIMMYGTLDPCWEKTIARDEGGKAFPIGAMSNVLRMGAGAPVLVLYDEIKKYT 298

Db 241 QSGRGKGTIMMYGTLDPCWEKTIARDEGGKAFPIGAMSNVLRMGAGAPVLVLYDEIKKYT 298

RESULT 2		
ID	Q8JH10	
	PRELIMINARY;	PRT; 298 AA.
Q8JH10.		
Q8JH10.		
DT	01-OCT-2002 (TREMBLrel. 22, Created)	
DT	01-OCT-2002 (TREMBLrel. 22, last annotation update)	
DT	01-MAR-2003 (TREMBLrel. 23, last annotation update)	
DE	Solute carrier family 25 member 5 protein.	
GN	SLC25A5.	
OS	Brachydanio rerio (zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
CC	Cyprinidae; Danio.	
OK	NCBI_taxid=7935;	
RV	[1]	
RV	SEQUENCE FROM N.A.	
RP	MEDLINE=22035902; PubMed=12006978;	
RA	Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,	
RA	Burgess S., Haldt M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,	
RA	Hopkins N.;	
RT	"Insertional mutagenesis in zebrafish rapidly identifies genes	
RT	essential for early vertebrate development.";	
RL	Nat. Genet. 31:135-140(2002).	
RL	EMBL; AF506216; AAM3460.1; -	
DR	InterPro; IPR001993; Mitoch_carrier.	
DR	InterPro; IPR002067; Mit_carrier.	
DR	InterPro; IPR002030; Mit_uncoupling.	
DR	Pfam; PF00153; mito_carr1_3.	
DR	PRINTS; PR00926; MITOCARRIER.	
DR	PRINTS; PR00784; MTUNCOUPLING.	
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.	
Q0	SEQUENCE 298 AA; 32763 MW; D70663CF65C5ID39 CRC64;	

	Query Match	93.7%;	Score 1450;	DB 13;	Length 298;
	Best Local Similarity	92.9%;	Pred. No. 3e-120;		
Matches	275;	Conservative	13;	Mismatches	8; Indels 0; Gaps 0
QY	1	MTDALSAPKDDLAGVAALISKTAVPLERVLTLLIQVHASKQIRADKKOYKEIIDCYVR	60		
Dd	1	MSEITLSPAKDDLAGGIAAISKTAAPIERVLTLLQVHASKQIRADKKOYKEIMCCVR	60		
QY	61	IPKEGEVLSPMRGNLANVIKYEPPTQALNFAFDKXKQIFLGVDKDTQFWRYPAGNIASG	120		
Dd	61	IPKEGGFLSPMRGNLANVIKYEPPTQLANFAFDKXKCVFLDGVDKDTQFWRYPAGNIASG	120		
QY	121	GAAGSTSLCFPVLPDPARTRLAADYGAAREEFGSGICVIKYISDDIGKIYGOFNNS	180		
Dd	121	GAAGSTSLCFVPLEDPARTRLAADYGAAREEFSGSGLCNLVKISDDIGKIYOGFNNS	180		
QY	181	VQGIIYYRAAYEGIVDTAKGMLPDPKNTHIVISMIAQTVTATAVAGLSYFPDTRRRMM	240		
Dd	181	VQGIITYRAAYEGIVDTAKGMLPDPKNTHIVYSMMAQSIVTATAVAGLSYFPDTRRRMM	240		
QY	241	OSGRGCTIMTYGLTDCKRKIARDDEGKAFFPGAWNNYLRMCGAGATVLVLYIDEIK	296		
Dd	241	OSGRGAIMTMSGLTDCWKRIARDDEGKAFFPGAWNNVLRMGAGATVLVLYIDELK	296		

00PRH1; 298 AA; 33054 MW; B0523AD56F548D36 CRC64;  
 01 MAY-2000 (T-EMBLrel. 13, Created)  
 01 MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 01 MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 ADP/ATP translocase.  
 OS Rana rugosa (Wrinkled frog).  
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.  
 NCBI\_TaxId=8410;  
 [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=98083429; PubMed=9866197;  
 RA Mura I.; Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;  
 RT "The origin and differentiation of the heteromorphic sex chromosomes  
 z, w, x, and y in the frog *Rana rugosa*, inferred from the sequences of  
 a sex-linked gene, ADP/ATP translocase",  
 Mol. Biol. Evol. 15:1612-1619(1998).  
 CC -1. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AB008463; BA36513.1; -;  
 DR EMBL; AB008456; BA36506.1; -;  
 DR EMBL; AB008461; BA36511.1; -;  
 DR EMBL; AB008462; BA36512.1; -;  
 DR InterPro: IPR001993; Mitoch carrier.  
 DR InterPro: IPR002067; Mt carrier.  
 DR InterPro: IPR002030; Mt uncoupling.  
 DR Pfam; PF00153; mtco\_carrt\_3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SEQUENCE 298 AA; 33054 MW; B0523AD56F548D36 CRC64;

Query Match	Similarity	93.5%	Score 1446	DB 13	Length 298
Best Local	Similarity	91.9%	Pred. No. 6.8e-120		
Matches 273	Conservative	14	Mismatches 10	Indels 0	Gaps 0
Qy	1	MTDAALSPADQFLAGVVAALSKTAVAPIERHVKLLQVQHASKOITTDROYKGIIDCVRR	60		
Db	1	MTDAALSPADQFLAGVVAALSKTAVAPIERHVKLLQVQHASKOITTDROYKGIIDCVRR	60		
Qy	61	IPKEOVLSPWRGNLANVIRYPTQALNFAKDYKQIFLGVDKRTQFWRYFAGNTLASG	120		
Db	61	IPKEGVSPWRGNLANVIRYPTQALNFAKDYKQIFLNDVKRTQFWRYFAGNTLASG	120		
Qy	121	GAAGATSLCFEYPLDIPARTRLADVGKGAERERGLADCLVKLYKSGIKGLVGFENVIS	180		
Db	121	GAAGATSLCFEYPLDIPARTRLADVGKGAERERGLADCLVKLYKSGIKGLVGFENVIS	180		
Qy	181	VQGIIRAAAFGLYDPAKGM.LPDKNTHTIYISMNIQTVAVAGLSTYPRDYRRMM	240		
Db	181	VQGIIRAAAFGLYDPAKGM.LPDKNTHTIYISMNIQTVAVAGLSTYPRDYRRMM	240		
Qy	241	QSGRKQNDIMVTGLD.CWRKLARDGGKAFPKGAMSNVLRMGAFVLYLVDKIKY	297		
Db	241	QSGRKGRIMVSGTIIDCKKLARDGGSAFPKGMASNVLRMGAFVLYLVDKIKY	297		

RESULT	4
Q9PRH2	
ID	Q9PRH2
AC	Q9PRH2;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	ADP/ATP translocase.
OS	Rana rugosa (Wrinkled frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana
OX	NBI_TaxID=8410;
RN	[1]
RP	SEQUENCE FROM N.A.
EX	MEDLINE=99083429; PubMed=9866197;
RA	Mura I., Ontani H., Nakamura M., Ichikawa Y., Saitoh K.;

RT "The origin and differentiation of the heteromorphic sex chromosomes  
 RT z, w, x, and y in the frog *Rana rugosa*, inferred from the sequences of  
 RT a sex-linked gene, ADP/ATP translocase.";  
 RL Mol. Biol. Evol. 15:1612-1619(1998).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AB008460; BAA36510.1; -  
 DR EMBL; AB008458; BAA36508.1; -  
 DR EMBL; AB008459; BAA36509.1; -  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MITOUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 33082 MW; BOB225E867599A06 CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;  
 Best Local Similarity 91.6%; Pred. No. 1.2e-119;  
 Matches 272; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDAAISFADPFLAGVAAAIKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60  
 DB 1 MTDAAISFADPFLAGVAAAIKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60  
 QY 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDRKTOFWRYFAGNLASG 120  
 DB 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDRKTOFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGREBERGIGDCLVKIKSGDKIGLYQGFNV 180  
 DB 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGREBERGIGDCLVKIKSGDKIGLYQGFNV 180  
 QY 181 VQGIITIRAAVFGIYDTAKGMLDPPKNTHTIVISWMLAQVTAVAGLTSYPPDYRRRMM 240  
 DB 181 VQGIITIRAAVFGIYDTAKGMLDPPKNTHTIVISWMLAQVTAVAGLTSYPPDYRRRMM 240  
 QY 241 QSGRKGTDIMYTGTLDCWKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 297  
 DB 241 QSGRKGADIMYSGTIDCWKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 297

RESULT 5  
 Q8AYM3 PRELIMINARY; PRT; 298 AA.  
 AC Q8AYM3;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE ATP/ADP antiporter.  
 GN AVANT.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;  
 RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP  
 RT and ANT mRNA in chicken skeletal muscle.";  
 RL FEBS Lett. 0:0-0(2002).  
 DR EMBL; AB088686; BAC15533.1; -  
 SQ SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;  
 Best Local Similarity 92.9%; Pred. No. 1.2e-119;  
 Matches 275; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 MTDAAISFADPFLAGVAAAIKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60  
 DB 1 MTDAAISFADPFLAGVAAAIKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60

QY 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDRKTOFWRYFAGNLASG 120  
 DB 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDRKTOFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGREBERGIGDCLVKIKSGDKIGLYQGFNV 180  
 DB 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGREBERGIGDCLVKIKSGDKIGLYQGFNV 180  
 QY 181 VQGIITIRAAVFGIYDTAKGMLDPPKNTHTIVISWMLAQVTAVAGLTSYPPDYRRRMM 240  
 DB 181 VQGIITIRAAVFGIYDTAKGMLDPPKNTHTIVISWMLAQVTAVAGLTSYPPDYRRRMM 240  
 QY 241 QSGRKGTDIMYTGTLDCWKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 296  
 DB 241 QSGRKGADIMYSGTIDCWKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 296

RESULT 6  
 Q9YTC4 PRELIMINARY; PRT; 298 AA.  
 ID Q9YTC4;  
 AC Q9YTC4;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS *Rana rugosa* (Wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=9083429; PubMed=9866197;  
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;  
 RT "The origin and differentiation of the heteromorphic sex chromosomes  
 RT z, w, x, and y in the frog *Rana rugosa*, inferred from the sequences of  
 RT a sex-linked gene, ADP/ATP translocase.";  
 RL Mol. Biol. Evol. 15:1612-1619(1998).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AB008457; BAA36507.1; -  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MITOUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 93.0%; Score 1439; DB 13; Length 298;  
 Best Local Similarity 91.2%; Pred. No. 2.8e-119;  
 Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDAAISFADPFLAGVAAAIKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60  
 DB 1 MTDAAISFADPFLAGVAAAIKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60  
 QY 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDRKTOFWRYFAGNLASG 120  
 DB 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDRKTOFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGREBERGIGDCLVKIKSGDKIGLYQGFNV 180  
 DB 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGREBERGIGDCLVKIKSGDKIGLYQGFNV 180  
 QY 181 VQGIITIRAAVFGIYDTAKGMLDPPKNTHTIVISWMLAQVTAVAGLTSYPPDYRRRMM 240  
 DB 181 VQGIITIRAAVFGIYDTAKGMLDPPKNTHTIVISWMLAQVTAVAGLTSYPPDYRRRMM 240  
 QY 241 QSGRKGTDIMYTGTLDCWKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 297  
 DB 241 QSGRKGADIMYSGTIDCWKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 297

## RESULT 7

ID Q919M9 PRELIMINARY; PRT; 298 AA.

AC Q919M9 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Adenine nucleotide translocase.

CN ANTL.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

CX NCBI\_TaxID=83355;

RN [1]

RP SEQUENCE FROM N.A.

RA Crawford M.J., Kiosrowshanian F., Varmuza S.L., Liverage R.A.;

RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and

RT Dynamic Patterns of Expression During Development.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AF21347; AAF63471.1; -.

DR InterPro; IPR001993; Mitoch\_carrier.

DR InterPro; IPR002067; Mlt\_carrier.

DR InterPro; IPR002030; Mlt\_uncoupling.

DR Pfam; PF00153; mltc\_carr; 3.

DR PRINTS; PR00926; MITOCARRIER.

DR PRINTS; PR00784; MTNOCOUPLING.

DR PROSITE; PS00215; MITOCH\_CARRIER; 3.

DR Membrane; Transmembrane; Transport.

SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 92.1%; Score 1425; DB 13; Length 298;  
Best Local Similarity 91.6%; Pred. No. 4,9e-118;  
Matches 271; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSAKDFLAGGVAALSKTAVAPIERVKLLQVOHASKOTTADKOYKGIIDCVR 60

DB 1 MTDALSAKDFLAGGVAALSKTAVAPIERVKLLQVOHASKOTTADKOYKGIIDCVR 60

QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120

DB 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120

QY 121 GAAGTSLCFYVPLDPARTRLAADVGKAGAREPGLDCLVTKYKSGIKGLYOGFNVS 180

DB 121 GAAGTSLCFYVPLDPARTRLAADVGKAGAREPGLDCLVTKYKSGIKGLYOGFNVS 180

QY 121 GAAGTSLCFYVPLDPARTRLAADVGKAGAREPGLDCLVTKYKSGIKGLYOGFNVS 180

DB 121 GAAGTSLCFYVPLDPARTRLAADVGKAGAREPGLDCLVTKYKSGIKGLYOGFNVS 180

QY 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVISMMIAQTVAAGLTSYPPDVTARRMM 240

DB 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVISMMIAQTVAAGLTSYPPDVTARRMM 240

QY 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVISMMIAQTVAAGLTSYPPDVTARRMM 240

DB 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVISMMIAQTVAAGLTSYPPDVTARRMM 240

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 296

RC TISSUE=Skeletal muscle;

RA Yamaguchi N., Kasai M.;

RT "Identification of a 30kDa calsequestrin-binding protein, which

RT regulates calcium release from sarcoplasmic reticulum of rabbit

RT skeletal muscle.";

RL J. Biochem. 335:541-547(1998).

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AB009386; BAA23777.1; -.

DR InterPro; IPR001993; Mitoch\_carrier.

DR InterPro; IPR002067; Mlt\_carrier.

DR InterPro; IPR002030; Mlt\_uncoupling.

DR Pfam; PF00153; mltc\_carr; 3.

DR PRINTS; PR00926; MITOCARRIER.

DR PRINTS; PR00784; MTNOCOUPLING.

DR PROSITE; PS00215; MITOCH\_CARRIER; 3.

DR Membrane; Transmembrane; Transport.

SQ SEQUENCE 298 AA; 32901 MW; CABA32C88164AD78 CRC64;

Query Match 92.0%; Score 1423; DB 6; Length 298;  
Best Local Similarity 89.9%; Pred. No. 7,4e-118;  
Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSAKDFLAGGVAALSKTAVAPIERVKLLQVOHASKOTTADKOYKGIIDCVR 60

DB 1 MSDQSLFLKDFLAGGVAALSKTAVAPIERVKLLQVOHASKOTTADKOYKGIIDCVR 60

QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120

DB 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120

QY 121 GAAGTSLCFYVPLDPARTRLAADVGKAGAREPGLDCLVTKYKSGIKGLYOGFNVS 180

DB 121 GAAGTSLCFYVPLDPARTRLAADVGKAGAREPGLDCLVTKYKSGIKGLYOGFNVS 180

QY 121 GAAGTSLCFYVPLDPARTRLAADVGKAGAREPGLDCLVTKYKSGIKGLYOGFNVS 180

DB 121 GAAGTSLCFYVPLDPARTRLAADVGKAGAREPGLDCLVTKYKSGIKGLYOGFNVS 180

QY 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVISMMIAQTVAAGLTSYPPDVTARRMM 240

DB 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVISMMIAQTVAAGLTSYPPDVTARRMM 240

QY 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVISMMIAQTVAAGLTSYPPDVTARRMM 240

DB 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVISMMIAQTVAAGLTSYPPDVTARRMM 240

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

QY 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297

DB 241 QSGRKGADIMVTGTLDCKRKIARDEGKAFFKGANSNVLKMGAFVLYLDEIKY 297



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Db      1 MDKALSPKDLFLAGGAAVSKTAVAPIERVKLLQVQHASKOJSAEKQYGIIDCVR 60
Qy      1 PKGEVLSFMRGNLANVIRYPTQALNFAFDKXKQJFLGVDVDRTOFWRRFAANLASG 120
Db      61 IPKEGGLISFMRGNLANVIRYPTQALNFAFDKXKQJFLGVDVDRTOFWRRFAANLASG 120
Qy      121 GAAAGTSLCFYVPLDPFARTRLAADVGKAGAREFRGLDCLVKIKYSGDIKGLYOGFNV 180
Db      121 GAAAGTSLCFYVPLDPFARTRLAADVGKAGAREFRGLDCLVKIKYSGDIKGLYOGFNV 180
Qy      181 VGGIIIRYAAVFGYDIAKGMPLDPKNTPIVISMIAQTVTAVALGTSYPTVARRMM 240
Db      181 VGGIIIRYAAVFGYDIAKGMPLDPKNTPIVISMIAQTVTAVALGTSYPTVARRMM 240
Qy      241 OSGRKGTIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFTVLYDEIKKY 297
Db      241 OSGRKGTIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFTVLYDEIKKY 297

RESULT 10
ID      091336 PRELIMINARY; PRT; 317 AA.
AC      091336;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-MAR-1999 (TREMBLrel. 10, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      ADP/ATP translocase
OS      Rana sylvatica (Wood frog).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX      NCBI_TaxID=45438;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=97398141; PubMed=9256066;
RA      Cai Q., Greenway S.C., Storey K.B.;
RT      "Differential regulation of the mitochondrial ADP/ATP translocase gene
RL      in wood frogs under freezing stress.";
RN      Biochim. Biophys. Acta 1353:69-78(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RA      Cai Q., Storey K.B.;
RL      Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DB      EMBL; U44932; AAA97882.2; -.
DR      InterPro; IPR001993; Mitoch_carrier.
DR      Pfam; PF00153; mito_carrier.3.
DR      PRINTS; PR00926; MITOCARRIER.
DR      PROSITE; PS00215; MITOCH_CARRIER.3.
KM      Membrane; Transmembrane; Transport.
SQ      SEQUENCE 317 AA; 35005 MW; 5F6B7EDBD5CEB72 CRC64;

Query Match      83.7%; Score 1295; DB 13; Length 317;
Best Local Similarity 90.1%; Pred. No. 1.7e-106;
Matches 245; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

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Qy      241 OSGRKGTIMYTGTLDCWKRKLARDGKGAFFK 272
Db      241 OSGRKGTIMYTGTLDCWKRKLARDGKGAFFR 272

RESULT 11
ID      095VX4 PRELIMINARY; PRT; 299 AA.
AC      095VX4;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      ADP-ATP translocator.
OS      Ethmostigmus rubripes.
OC      Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC      Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX      NCBI_TaxID=62613;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Burnell J.N.;
RT      "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RL      rubripes.";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF401758; AAL02100.1; -.
DR      InterPro; IPR001993; Mitoch_carrier.
DR      InterPro; IPR002067; Mit_carrier.
DR      Pfam; PF00153; mito_carrier.3.
DR      PRINTS; PR00926; MITOCARRIER.
DR      PROSITE; PS00215; MITOCH_CARRIER.3.
SQ      SEQUENCE 299 AA; 33037 MW; 3C3B8CB267C3C58 CRC64;

Query Match      82.6%; Score 1278; DB 5; Length 299;
Best Local Similarity 82.8%; Pred. No. 5.2e-105;
Matches 241; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

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Qy      5 ALSPKQPLAGVAAISKTAVAPIERVKLLQVQHASKOTIADKQYGIIDCVRRPKE 64
Db      5 AVSPKQPLAGVAAISKTAVAPIERVKLLQVQHASKOTIADKQYGVADCFVRRPQE 64
Qy      65 QEVLSFMRGNLANVIRYPTQALNFAFDKXKQJFLGVDVDRTOFWRRFAANLASG 124
Db      65 QGIIISYMRGNLANVIRYPTQALNFAFDKXKQJFLGVDVDRTOFWRRFAANLASG 124
Qy      125 ATSLCFYVPLDPFARTRLAADVGKAGAREFRGLDCLVKIKYSGDIKGLYOGFNV 184
Db      125 ATSLCFYVPLDPFARTRLAADVGKAGAREFRGLDCLVKIKYSGDIKGLYOGFNV 184
Qy      185 IYRAAAYFGYDIAKGMPLDPKNTPIVISMIAQTVTAVALGTSYPTVARRMM 244
Db      185 IYRAAAYFGYDIAKGMPLDPKNTPIVISMIAQTVTAVALGTSYPTVARRMM 244
Qy      245 KGTIDIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFTVLYDEIK 295
Db      245 KKAIDILKNTIDCWGKIKYKTEGGAFFKGAASNTLRGGAFTVLYDEIK 295

RESULT 12
ID      081RA0 PRELIMINARY; PRT; 312 AA.
AC      081RA0;
DT      01-MAR-2003 (TREMBLrel. 23, Created)
DT      01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      CG16944-PC.
GN      SEGB.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.

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RA MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton R.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abill J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter A.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Doudon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foaier C., Garbalian A.E., Gary N.S., Gelbart W.M., Glaeser K.,  
 RA Gload K., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hoeltin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,  
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Laevo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Maitzel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Modarres C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*.";  
 RA Science 287:2185-2195 (2000).  
 [2]  
 RA SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banton J., An H., Baldwin D., Banton J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorssett V., Doup L.E., Doyle C., Dreenek D., Farfan D.,  
 RA Ferreira S., Frise E., Galie R.F., Gary N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ingewald T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA McIntosh T.C., Mays A., Mays A.D., Mays A.D., Mays A.D.,  
 RA Pacle J.M., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RA "Sequencing of *Drosophila melanogaster* genome.";  
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 [3]  
 RA SEQUENCE FROM N.A.  
 RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
 RA Tupy J.L., Begman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clump W., Drysdale R., Emmert D., Frise B., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RA "Annotation of *Drosophila melanogaster* genome.";  
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 [4]  
 RA SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;  
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 [5]  
 RA SEQUENCE FROM N.A.

RA FlyBase;  
 RA Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.  
 RA EMBL; AE003484; AAN09267.1;  
 RA SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;  
 SQ  
 Query Match 81.0%; Score 1253.5; DB 5; Length 312;  
 Beest Local Similarity 81.2%; Pred. No. 8.1e-103;  
 Matches 237; Conservative 21; Mismatches 33; Indels 1; Gaps 1;  
 Oy 5 A L S F A K D L A G V A A A I S K T A V A P E R V K L L Q V H A S K Q I T A D K Q Y G A I I D C V R I P K E 64  
 Db A V G F Y K D P A A G I S A A V K T A V A P E R V K L L Q V H I S K Q I S P D K Q Y G M D C F R I P K E 79  
 Oy 65 Q E V L S F W R G N T A N V I R Y P P T O A L N F A F D K Y K Q I F L G V D K R T Q F W R Y P A G N L A S G A A G 124  
 Db O G F S S F W R G N T A N V I R Y P P T O A L N F A F D K Y K Q V E L G V D K N T Q F W R Y P A G N L A S G A A G 139  
 Oy 125 A T S I C F V Y P L D P A R T R L A A D V G K A E E P F L D D C V I K Y S D I K G L Y O G F N V S Y O G I 184  
 Db A T S I C F V Y P L D P A R T R L A A D T G K - G G Q R E F T G L G N C L T K I R S D E I V G L Y R G F V S Y O G I 198  
 Oy 185 I I Y R A A Y F G I Y D T A K G M L P D E K N T H I V S M M I A O T V T A V A G L T S Y P F D T V R R M M O S G R 244  
 Db I I Y R A A Y G F D T A R G M L P D K N T P I Y S M A I A V T T V A G I V S F P F T V R R M M O S G R 258  
 Oy 245 K G T D I M Y T G T L D C R K T A R D E G K A F F K G A N S V I R G M G A F V L Y D E I T K 296  
 Db K A T E V I Y K N T L H C W A T I A K Q R G T G A F F K G A F S N I L R G T G A F V L Y D E I T K 310  
 RESULT 13  
 ID Q9NHWS PRELIMINARY; PRT; 300 AA.  
 GNHWS  
 AC Q9NHWS; 15.  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Lucilia.  
 CC NCBI\_TaxID=7375;  
 [1]  
 RA SEQUENCE FROM N.A.  
 RA STRAIN=SS mal seeking;  
 RA Chen Z., Fair J.A., Baxterham P.;  
 RA "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*.";  
 RA Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 CC EMBL; AF218587; AAF2322.1;  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR InterPro; IPR002067; Mit carrier.  
 DR Pfam; PF00153; mltc\_carr\_3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;  
 Query Match 80.7%; Score 1248.5; DB 5; Length 300;  
 Beest Local Similarity 81.2%; Pred. No. 2.1e-102;  
 Matches 237; Conservative 20; Mismatches 34; Indels 1; Gaps 1;  
 Oy 6 L S F A K D L A G V A A A I S K T A V A P E R V K L L Q V H A S K Q I T A D K Q Y G A I I D C V R I P K E 65  
 Db L G F Y K D P A A G I S A A V K T A V A P E R V K L L Q V H I S K Q I S P D K Q Y G M D C F R I P K E 68  
 Oy 66 E V L S F W R G N T A N V I R Y P P T O A L N F A F D K Y K Q I F L G V D K R T Q F W R Y P A G N L A S G A A G 125  
 Db G F A S Y W R G N T A N V I R Y P P T O A L N F A F D K Y K Q V E L G V D K N T Q F W R Y P A G N L A S G A A G 128  
 Oy 126 T S L C F V Y P L D P A R T R L A A D V G K A E E P F L D D C V I K Y S D I K G L Y O G F N V S Y O G I 185

Db 129 TSLCFVYPLDPAFRTLAADTGK-GGQREFTGLGNCIAKIFKSDGLVGLRGVSVGCI 187  
 Qy 186 IYRAAYFPIYDTAKGMLPDPKNTHTVISMIAQTVAAGLTSYFPDVRMMQSGRK 245  
 Db 188 IYRAAYFPIYDTAKGMLPDPKNTHTVISMIAQTVAAGLTSYFPDVRMMQSGRK 247  
 Qy 246 GTDIWYTGTLDCWKRIARDEGKAFPKGAMSVNLGKGAFAVLVYDEIKKY 297  
 Db 248 ATETIYKNTLHCWATIAKQEGTGAFFKGAFSNVLRTGTGAFLVYDEIKKY 299

## RESULT 14

044093 PRELIMINARY: PRT: 288 AA.

AC 044093  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE ADP/ATP translocase (Fragment).  
 GN SESH.  
 OS Drosophila pseudoobscura (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 CX NCBI\_Taxid=7237;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.,  
 RL Genetics 0:0-0(1997).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AF025799; AAB87884.1; -.  
 DR FlyBase: FBgn0023292; Dpse\seeb.  
 DR InterPro: IPR001993; Mitoch\_carrier.  
 DR InterPro: IPR002067; Mit\_carrier.  
 DR Pfam: PF00153; mito\_carr; 3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PROSITE: PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Repeat; Transmembrane; Transport.  
 FT NON\_TER 288  
 SQ SEQUENCE 288 AA; 31725 MW; 052B0CC005043680 CRC64;

Query Match 77.0%; Score 1190.5; DB 5; Length 288;  
 Best Local Similarity 80.4%; Pred. No. 2.8e-97;  
 Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

Qy 5 ALSFAKDFLAGVAAIAIKTAVAPIERVKLLQVOHASKQITADKQYGIIDCVIRIPKE 64  
 Db 7 AIGFVKDFPAAGGISAASVKTAIVAPIERVKLLQVOHASKQISPDKQYGMVDCFRIPKE 66  
 Qy 65 QEVLSFMRGNLANVIRYPTQALNPAFDKTKQIFLGVDKRTQFWRFPAGNLASGGAG 124  
 Db 67 QGFSSFMKGNLANVIRYPTQALNPAFDKTKQIFLGVDKRTQFWRFPAGNLASGGAG 126  
 Qy 125 ATSLCFVYPLDPAFRTLAADVGKAGREBFGDCLVKIYKSDGIKGLYOGFNVSVOGI 184  
 Db 127 ATSLCFVYPLDPAFRTLAADVGK-GGQREFTGLGNCIAKIFKSDGLVGLRGVSVGCI 185  
 Qy 185 IYRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAAGLTSYFPDVRMMQSGR 244  
 Db 186 IYRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAAGLTSYFPDVRMMQSGR 244  
 Qy 245 KGTIDMTGTLDCKWKRIARDEGKAFPKGAMSVNLGKGAFAVLV 289  
 Db 245 KATEIYKNTLHCWATIAKQEGTGAFFKGAFSNVLRTGTGAFLV 288

## RESULT 15

044094 PRELIMINARY: PRT: 288 AA.

AC 044094  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).

GN SESH.

OS Drosophila subobscura (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

CX NCBI\_Taxid=7241;

RN [1]

RP SEQUENCE FROM N.A.

RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;

RL Genetics 0:0-0(1997).

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL: AF025799; AAB87884.1; -.  
 DR FlyBase: FBgn0023237; Dsub\seeb.  
 DR InterPro: IPR001993; Mitoch\_carrier.  
 DR InterPro: IPR002067; Mit\_carrier.  
 DR Pfam: PF00153; mito\_carr; 3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PROSITE: PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Repeat; Transmembrane; Transport.  
 FT NON\_TER 288  
 SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.6%; Score 1185.5; DB 5; Length 288;  
 Best Local Similarity 80.0%; Pred. No. 7.7e-97;  
 Matches 228; Conservative 21; Mismatches 33; Indels 3; Gaps 3;

Qy 5 ALSFAKDFLAGVAAIAIKTAVAPIERVKLLQVOHASKQITADKQYGIIDCVIRIPKE 64  
 Db 7 AMGFVKDFPAAGGISAASVKTAIVAPIERVKLLQVOHASKQISPDKQYGMVDCFRIPKE 66  
 Qy 65 QEVLSFMRGNLANVIRYPTQALNPAFDKTKQIFLGVDKRTQFWRFPAGNLASGGAG 124  
 Db 67 QGFSSFMKGNLANVIRYPTQALNPAFDKTKQIFLGVDKRTQFWRFPAGNLASGGAG 126  
 Qy 125 ATSLCFVYPLDPAFRTLAADVGKAGREBFGDCLVKIYKSDGIKGLYOGFNVSVOGI 184  
 Db 127 ATSLCFVYPLDPAFRTLAADVGK-GGQREFTGLGNCIAKIFKSDGLVGLRGVSVGCI 185  
 Qy 185 IYRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAAGLTSYFPDVRMMQSGR 244  
 Db 186 IYRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAAGLTSYFPDVRMMQSGR 244  
 Qy 245 KGTIDMTGTLDCKWKRIARDEGKAFPKGAMSVNLGKGAFAVLV 289  
 Db 245 KATEIYKNTLHCWATIAKQEGTGAFFKGAFSNVLRTGTGAFLV 288

Search completed: December 18, 2003, 12:43:10  
 Job time : 31.701 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:36:16 / Search time 8.34267 Seconds  
(without alignments)  
1679.794 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543

Sequence: 1 MTEQALSPAKFLAGTAA.....LRGNGAFVLYVDELKVI 298

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	ADT3_HUMAN	P12236 homo sapien
2	1512	98.0	298	ADT3_BOVIN	P32007 bos taurus
3	1463	94.8	298	ADT2_HUMAN	P05141 homo sapien
4	1451	94.0	298	ADT2_RAT	Q09073 rattus norv
5	1445	93.6	298	ADT2_MOUSE	P51881 mus musculu
6	1424	92.3	298	ADT1_RAT	Q05962 rattus norv
7	1418	91.9	298	ADT1_MOUSE	P48962 mus musculu
8	1417	91.8	297	ADT1_BOVIN	P02722 bos taurus
9	1409	91.3	298	ADT1_HUMAN	P12335 homo sapien
10	1254.5	81.3	299	ADT_TKOME	Q26365 drosophila
11	1204	78.0	301	ADT_ANOGA	Q27238 anopheles g
12	978	63.4	339	ADT_CHLKE	P31692 chlorella k
13	778.5	50.5	307	ADT3_YEAST	P18238 saccharomyc
14	772	50.0	308	ADT_CHLKE	P27080 chlamydomon
15	769	49.8	322	ADT_SCHPO	Q09188 schizosacch
16	768	49.8	386	ADT1_GOSHI	O22342 gossepium h
17	766	49.6	313	ADT_NEUCR	P02723 neurospora
18	762.5	49.4	305	ADT_KULIA	P48382 kluyveromyc
19	760.5	49.3	318	ADT2_YEAST	P18239 saccharomyc
20	750	48.6	385	ADT2_ARATH	P48941 arabidopsis
21	750	48.6	387	ADT1_MAIZE	P46709 zea mays (m
22	748	48.5	386	ADT1_SOLTU	P25083 solanum tub
23	747	48.4	382	ADT_OXYSA	P18571 oxyza sativ
24	744	48.2	387	ADT2_MAIZE	P18571 oxyza sativ
25	742.5	48.0	381	ADT1_ARATH	P31167 arabidopsis
26	740	48.0	331	ADT1_WHEAT	Q41629 triticum ae
27	739.5	47.9	386	ADT2_SOLTU	P27081 solanum tub
28	737.5	47.8	309	ADT1_YEAST	P04710 saccharomyc
29	727	47.1	331	ADT2_WHEAT	Q41630 triticum ae
30	305.5	19.8	565	CMC3_CABEL	Q19529 caenorhabdi
31	302	19.6	588	CMC2_CABEL	Q20799 caenorhabdi
32	300	19.4	330	GDC_BOVIN	Q01888 bos taurus
33	299	19.4	307	ODC2_YEAST	Q99297 saccharomyc

34	295	19.1	678	1	CMC1_HUMAN	O75746 homo sapien
35	289.5	18.8	322	1	GDC_RAT	P16261 rattus norv
36	287.5	18.6	702	1	CMC1_CABEL	O21153 caenorhabdi
37	286	18.5	325	1	UCP5_HUMAN	O95258 homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260 homo sapien
39	284	18.4	325	1	UCP5_MOUSE	Q922b2 mus musculu
40	282.5	18.3	326	1	YCB8_SCHPO	O13805 schizosacch
41	280	18.1	675	1	CMC2_HUMAN	Q91560 homo sapien
42	272	17.6	315	1	MPT_HUMAN	O912d1 homo sapien
43	270	17.5	315	1	SH18_HUMAN	Q911k4 homo sapien
44	265	17.2	312	1	UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676	1	CMC2_MOUSE	Q9qxx4 mus musculu

## ALIGNMENTS

RESULT 1  
ADT3\_HUMAN STANDARD; PRT; 298 AA.  
AC P12236; Q96C49;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)  
DE (Adenine nucleotide translocator 3) (ANT 3).  
GN SLC25A6 OR ANT3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Metazoa; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89236396; PubMed=2541251;  
RA Cozens A.L., Runswick M.J., Walker J.B.;  
RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
ADP/ATP translocase.";  
RL J. Mol. Biol. 206:261-280(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
Margolin J.F.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, Cervix, Eye, and Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Dichtchenko L., Marudina K., Farmer A.A., Rudin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
Raba S.S., Loggellano N.A., Peters G.J., Johnson R.D., Mullaly S.J.,  
Bosak S.A., McMan P.U., McKernan K.J., Malek J.A., Gutarra P.H.,  
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.B.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP SEQUENCE OF 36-298 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=88124845; PubMed=2829183;  
RA Houldsworth J., Attardi G.;  
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

RT level in adult human liver.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC -----  
 CC EMBL, J03592; AAA36750.1; -;  
 DR EMBL, AY007135; AAG01998.1; -;  
 DR EMBL, BC007295; AAH07295.1; -;  
 DR EMBL, BC007850; AAH07850.1; -;  
 DR EMBL, BC008737; AAH08737.1; -;  
 DR EMBL, BC008935; AAH08935.1; -;  
 DR EMBL, BC014775; AAH14775.1; -;  
 DR PIR, S03894; S03894.  
 DR Genew; HGNC:10992; SLC25A6.  
 DR MIM, 300151; -;  
 DR MIM, 403000; -;  
 DR GO, GO:0005744; C:mitochondrial inner membrane translocase co. .; TMS.  
 DR GO, GO:0005471; P:ATP/ADP antiporter activity; NAS.  
 DR GO, GO:0006854; P:ATP/ADP exchange; TMS.  
 DR InterPro; IPR002067; Mlt carrier.  
 DR InterPro; IPR002030; Mlt uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carri; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 100 1.  
 FT REPEAT 101 208 2.  
 FT REPEAT 209 298 3.  
 FT REPEAT 299 328 4.  
 FT CONFLICT 105 108 KTO -> RHA (IN REF. 4).  
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).  
 SQ SEQUENCE 298 AA; 32866 MW; 1853489F0E4672F CRC64;  
 Query Match 100.0%; Score 1543; DB 1; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-128;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 MTEQAISPAKDFLAGIAAIAISKTAAPVPIERVKLLQVOHASKQIAADKOYGIYDCLVR 60  
 Db 1 MTEQAISPAKDFLAGIAAIAISKTAAPVPIERVKLLQVOHASKQIAADKOYGIYDCLVR 60  
 Oy 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHKTOFWRYFAGNLASG 120  
 Db 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHKTOFWRYFAGNLASG 120  
 Oy 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHKTOFWRYFAGNLASG 120  
 Db 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHKTOFWRYFAGNLASG 120  
 Oy 121 GAAGTSTLCFYPPDPAFTRLAADVKGSTEREPGLDCLVTKSGIKGLYGGSEVS 180  
 Db 121 GAAGTSTLCFYPPDPAFTRLAADVKGSTEREPGLDCLVTKSGIKGLYGGSEVS 180  
 Oy 121 GAAGTSTLCFYPPDPAFTRLAADVKGSTEREPGLDCLVTKSGIKGLYGGSEVS 180  
 Db 121 GAAGTSTLCFYPPDPAFTRLAADVKGSTEREPGLDCLVTKSGIKGLYGGSEVS 180  
 Oy 181 VGGIITTAAYFGVDTAKGMLPDKRNTIIVVSMIACTVAVAGVSVYPTVARRMM 240  
 Db 181 VGGIITTAAYFGVDTAKGMLPDKRNTIIVVSMIACTVAVAGVSVYPTVARRMM 240  
 Oy 181 VGGIITTAAYFGVDTAKGMLPDKRNTIIVVSMIACTVAVAGVSVYPTVARRMM 240  
 Db 181 VGGIITTAAYFGVDTAKGMLPDKRNTIIVVSMIACTVAVAGVSVYPTVARRMM 240

Oy 241 QSGRRKADIMTYGVDCWRKIFRDEGKAFPKGANSVLRMGAFVLVYDELKVI 298  
 Db 241 QSGRRKADIMTYGVDCWRKIFRDEGKAFPKGANSVLRMGAFVLVYDELKVI 298  
 RESULT 2  
 ID ADT3 BOVIN STANDARD; PRT; 298 AA.  
 AC P32007;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine  
 DE nucleotide translocator 3) (ANT 3).  
 DE SLC25A6 OR ANT3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RP [1]  
 RX MEDLINE=89223093; PubMed=2540808;  
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;  
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed  
 RT differences in various tissues."  
 RL Biochemistry 28:866-873(1989).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC -----  
 CC EMBL, M24103; AAA30769.1; -;  
 DR PIR, B43646; B43646.  
 DR InterPro; IPR002067; Mlt carrier.  
 DR InterPro; IPR002030; Mlt uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carri; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 100 1.  
 FT REPEAT 101 208 2.  
 FT REPEAT 209 298 3.  
 FT REPEAT 299 328 4.  
 SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6E8DE4061 CRC64;  
 Query Match 98.0%; Score 1512; DB 1; Length 298;  
 Best Local Similarity 97.7%; Pred. No. 1.9e-125;  
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 MTEQAISPAKDFLAGIAAIAISKTAAPVPIERVKLLQVOHASKQIAADKOYGIYDCLVR 60  
 Db 1 MTEQAISPAKDFLAGIAAIAISKTAAPVPIERVKLLQVOHASKQIAADKOYGIYDCLVR 60

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	DR	-----
	DR	EMBL; M57424; AAA51737.1; -
	DR	EMBL; J02683; AAA35579.1; -
	DR	EMBL; L78810; AAB39266.1; -
	DR	EMBL; AC004000; AAB96347.1; -
	DR	EMBL; J03591; AAA36749.1; -
	DR	PfR; A29132; A29132.
	DR	GeneW; HGNC:10991; SLC25A5.
	DR	MIM; 300150; -
	DR	GO; GO:0005867; C:integral to plasma membrane; TAS.
	DR	GO; GO:0015207; P:adenine transporter activity; TAS.
	DR	GO; GO:0006832; P:sml molecule transport; TAS.
	DR	InterPro; IPR002067; Mt carrier.
	DR	InterPro; IPR002030; Mt uncoupling.
	DR	InterPro; IPR001993; Mitoch_carrier.
	DR	Pfam; PF00153; mito_carr; 3.
	DR	PRINTS; PR00326; MITOCARRIER.
	DR	PRINTS; PR00784; MTNCOUPLING.
	DR	PROSITE; PS00215; MITOCH_CARRIER; 3.
	KV	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
	KV	Multiqc family.
	FT	TRANSMEM 12            29         1 (POTENTIAL)
	FT	TRANSMEM 73            91         2 (POTENTIAL)
	FT	TRANSMEM 117          134         3 (POTENTIAL)
	FT	TRANSMEM 176          195         4 (POTENTIAL)
	FT	TRANSMEM 214          231         5 (POTENTIAL)
	FT	TRANSMEM 273          291         6 (POTENTIAL)
	FT	REPEAT 1              111         1.
	FT	REPEAT 112            208         2.
	FT	REPEAT 209            298         3.
	FT	CONFLICT 6            6           V -> L (IN REF. 2).
	FT	CONFLICT 66           66           G -> B (IN REF. 2).
	FT	CONFLICT 111          111          R -> L (IN REF. 4 AND 5).
	FT	CONFLICT 162          162          V -> G (IN REF. 5).
	SO	SEQUENCE 298 AA; 32895 MW; F973C3AAD92C49D3 CRC64;
		Query Match            94.8%; Score 1463; DB 1; Length 298;
		Best Local Similarity 92.9%; Pred. No. 3.be-121;
		Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
Oy	1	MTBQALSPADDFLAGIAAISKTAVAPIRRYVLLOVOHASQIOADKDYKIYVCIVR 60
Dd	1	MTDAASVPADFPLAGVAALISKAAPRIERVKLLQVGHASKQITADKKYKIIIDCVR 60
Oy	61	IPKEGVLSFWRGNLANVIKYFFPTOLANFAPKDKYKOIFPGVDKTOFRFYRFGNLASG 120
Dd	61	IPKGGLVSFPGRNLNAVIRYFPTQLNPAPFKOKYKQIFLGVDKRTQFRFYRFGNLASG 120
Oy	121	GAAATSLCFYYPIADPAKTLADVGSGETEREERIGLGDCLVTIKTSDDGIRGIYOGEFSV 180
Dd	121	GAAATSLCFYYPIADPAKTLADVGSGEREERIGLDCLVTIKTSDDGIRGIYOGEFNVS 180
Oy	181	VGGIITIRAAVFVGYPDPAKGMLEDPENKTHLVSSMMTAQTATAVAGVVSYEPDVRRRMNM 240
Dd	181	VGGIITIRAAVFGLYPDAKMLEDPEKNTHLVISMMLAQYTATAVAGLTSTPFDTVRRRMNM 240
Oy	241	QSGRKGAADIWYTGTVDCWKRIFDDEGGKAFPKGAMSNVLRGMGCAFLVLYIDEIKK 296
Dd	241	QSGRKGTIDIMWTGLDCWKRIARDEGGKAFPKGAMSNVLRGMGCAFVLYLYIDEIKK 296
RESULT 4		
ADT2_RAT	ID	ADT2_RAT            STANDARD;            PRT;            298 AA.
AC	0009073;	
DT	01-FEB-1995	(Rel. 31, Created)



DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DR ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 DE (Adenine nucleotide translocator 2) (ANT 2).  
 NM SLC25A5 OR ANT2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SOURCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=94002161; PubMed=8399300;  
 RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;  
 RT "Isolation and characterization of cDNA clones and a genomic clone  
 encoding rat mitochondrial adenine nucleotide translocator.";   
 RL Biochim. Biophys. Acta 1152:192-196 (1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND  
 CC SKELETAL MUSCLE.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL, D12771; BAA02238.1; -  
 DR InterPro; IPR002067; Mtc\_carrier.  
 DR InterPro; IPR002030; Mtc\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mto\_carri; 3-  
 DR PRINTS; PR00784; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR MitoChondriion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987E9F35 CRC64;  
 Query Match 94.0%; Score 1451; DB 1; Length 298;  
 Best Local Similarity 91.9%; Pred. No. 4.3e-120;  
 Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MTEQAIIPKADFLAGGIAAIGKTAVAPFERVKLLQVGHAKQIADQYGYDCTVR 60  
 DB 1 MTDAAVSPAKDPLAGGVAAAIKTAAPLERYKLLQVGHAKQIADQYGYIDCVRR 60  
 QY 61 IPEKGVISFMRGNLANVIRYPTQALNFAFDKQYQIPLGGVDKHTQFMRFAAGNLASG 120  
 DB 61 IPEKGVISFMRGNLANVIRYPTQALNFAFDKQYQIPLGGVDKHTQFMRFAAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPAFRTLADYVSGSTEREFRGLGDLVTKSDSIRGLYOGFSVS 180  
 DB 121 GAAGATSLCFVYPLDPAFRTLADYVSGSTEREFRGLGDLVTKSDSIRGLYOGFSVS 180  
 QY 181 VGGIITIRAAAYGVYDTAKGMLPDKNTHIVVSMIAQTVTVAAGVVSFPDTRRRMM 240

DB 191 VGGIITIRAAAYGVYDTAKGMLPDKNTHIVVSMIAQSVTAAGLTSPDTRRRMM 240  
 QY 241 QSGRGADIMTYGVDCWRKIIFDEGGAFFKGASNYLRGNGAFVLYYDELK 296  
 DB 241 QSGRGADIMTYGVDCWRKIIFDEGGAFFKGASNYLRGNGAFVLYYDEIKK 296  
 RESULT 5  
 ADT2 MOUSE STANDARD; PRT; 298 AA.  
 ID PS1881; O61311;  
 AC 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 DE (Adenine nucleotide translocator 2) (ANT 2).  
 NM SLC25A5 OR ANT2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SOURCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=97059403; PubMed=8903724;  
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;  
 RT "Rapid evolution of human pseudoautosomal genes and their mouse  
 RT homologs".  
 RL Mamm. Genome 7:25-30 (1996).  
 RN [2]  
 RP SOURCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RA Sheldon J.G.;  
 RL Sheils (1995), University of Cambridge, U.K.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv;  
 RA Coslett P., Laplace C.;  
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP REVISIONS.  
 RA Laplace C.;  
 RL Labeled (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20432087; PubMed=10974536;  
 RA Levy S.B., Chen Y.-S., Graham B.H., Wallace D.C.;  
 RT "Expression and sequence analysis of the mouse adenine nucleotide  
 RT translocase 1 and 2 genes".  
 RL Gene 254:57-66 (2000).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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 CC -----  
 DR EMBL, U27316; AAC52838.1; -  
 DR EMBL, U10404; AAA19009.1; -  
 DR EMBL, X70847; CAA50196.1; -  
 DR EMBL, AF240003; AAF64471.1; -  
 DR MGI; MGI:1353496; SLC25A5.  
 DR InterPro; IPR002067; Mtc\_carrier.

DR InterPro: IPR002030; Mit uncoupling.  
 DR InterPro: IPR001993; Mitoch carrier.  
 DR Pfam: PF00153; mito\_carr; 3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PROSITE: PS00784; MITOC CARRIER.  
 DR PROSITE: PS00215; MITOCH CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 MultiGene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 FT SEQUENCE 298 AA; 32931 MW; 0798B04B987BFE20 CRC64;

Query Match 93.6%; Score 1445; DB 1; Length 298;  
 Best Local Similarity 91.6%; Pred. No. 1.4e-119;  
 Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGGIAAIAISKTAIVAPIERVKLLQVOHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MTDAAVSPKDFLAGGVAIAISKTAIVAPIERVKLLQVOHASKOITADKQYKGIIVDCIVR 60  
 QY 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKHTQFMWYFAGNLASG 120  
 DB 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKHTQFMWYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPAFTRILAAADVGSKSTEREPFGDCLVKTGSGIGLQGSFVS 180  
 DB 121 GAAGATSLCFVYPLDPAFTRILAAADVGSKSTEREPFGDCLVKTGSGIGLQGSFVS 180  
 QY 181 VQGIITRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPPTVRRMM 240  
 DB 181 VQGIITRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPPTVRRMM 240  
 QY 241 QSGRKGADIMYTGVDICWRKIARDEGSKAFPGKAMSVNLKMGAFVLVYDEIKKY 298  
 DB 241 QSGRKGADIMYTGVDICWRKIARDEGSKAFPGKAMSVNLKMGAFVLVYDEIKKY 298

RESULT 6  
 ADT1 RAT STANDARD; PRT; 298 AA.

AC Q05962;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP  
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
 GN SLC25A4 OR ANT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;  
 RX MEDLINE=94002161; PubMed=8399300;  
 RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;  
 RT "Isolation and characterization of cDNA clones and a genomic clone  
 RT encoding rat mitochondrial adenine nucleotide translocator";  
 RL Biochem. Biophys. Acta 1152:192-196(1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER  
 CC EXTENT, IN BRAIN AND KIDNEY.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
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DR EMBL: X61667; CA43842.1; -;  
 DR EMBL: D12770; BAA02337.1; -;  
 DR PIR: I60173; I60173.  
 DR InterPro: IPR002067; Mit carrier.  
 DR InterPro: IPR002030; Mit uncoupling.  
 DR InterPro: IPR001993; Mitoch carrier.  
 DR Pfam: PF00153; mito\_carr; 3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PROSITE: PS00784; MITOCH CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 MultiGene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 110 1.  
 FT REPEAT 111 208 2.  
 FT REPEAT 209 298 3.  
 FT SEQUENCE 298 AA; 32989 MW; 66704F78C6C320 CRC64;

Query Match 92.3%; Score 1424; DB 1; Length 298;  
 Best Local Similarity 89.6%; Pred. No. 1e-117;  
 Matches 267; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGGIAAIAISKTAIVAPIERVKLLQVOHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MGDQALSFKDFLAGGIAAIAISKTAIVAPIERVKLLQVOHASKOISAEKQYKGIIVDCIVR 60  
 QY 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKHTQFMWYFAGNLASG 120  
 DB 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKHTQFMWYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPAFTRILAAADVGSKSTEREPFGDCLVKTGSGIGLQGSFVS 180  
 DB 121 GAAGATSLCFVYPLDPAFTRILAAADVGSKSTEREPFGDCLVKTGSGIGLQGSFVS 180  
 QY 181 VQGIITRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPPTVRRMM 240  
 DB 181 VQGIITRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPPTVRRMM 240  
 QY 241 QSGRKGADIMYTGVDICWRKIARDEGSKAFPGKAMSVNLKMGAFVLVYDEIKKY 298  
 DB 241 QSGRKGADIMYTGVDICWRKIARDEGSKAFPGKAMSVNLKMGAFVLVYDEIKKY 298

RESULT 7  
 ADT1 MOUSE STANDARD; PRT; 298 AA.

AC P48962; Q62164;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP  
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).  
 GN SLC25A4 OR ANT1 OR ANCI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;

[1] SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6; TISSUE=Brain;  
 RC MEDLINE=97059403; PubMed=8903724;  
 RX Ellison J.W., Li X., Francke U., Shapiro L.J.;  
 RA "Rapid evolution of human pseudautosomal genes and their mouse  
 homologs.";  
 RT Mamm. Genome 7:25-30(1996).  
 RL  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Muscle;  
 RA Laplace C., Costet P.;  
 RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Levy S.B., Chen Y.-S., Graham B.H., Wallace D.C.;  
 RT "Expression and sequence analysis of the mouse adenine nucleotide  
 translocase 1 and 2 genes.";  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Cantucci P., Paege C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
 RA Boeck S.A., McKean P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.W.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 MITOCHONDRIAL INNER MEMBRANE.  
 CC  
 CC -1- SUBUNIT: Homodimer.  
 CC  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane.  
 CC  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC  
 CC EMBL, U27315; AAC52837.1; -;  
 DR EMBL, X74510; CAAS2616.1; -;  
 DR EMBL, AF240002; AAF64470.1; -;  
 DR EMBL, BC003791; AAH03791.1; -;  
 DR EMBL, BC026925; AAH26925.1; -;  
 DR PIR, S37210; S37210.  
 DR MGI, MGI:1353495; Slc25a4.  
 DR InterPro, IPR002067; Mlt\_carrier.  
 DR InterPro, IPR002030; Mlt\_uncoupling.  
 DR InterPro, IPR001993; Mitoch\_carrier.  
 DR Pfam, PF00153; mltcarr; 3.  
 DR PRINTS, PR000926; MITOCARRIER.  
 DR PRINTS, PR00784; MTUNCOUPLING.  
 DR PROSITE, PS00215; MITOCH\_CARRIER; 3.

KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 110 1.  
 FT REPEAT 111 208 2.  
 FT REPEAT 209 298 3.  
 FT CONFLICT 136 136 F -> L (IN REF. 1).  
 SQ SEQUENCE 298 AA; 32904 MM; 3A849FEA0981462 CAC64;  
 Query Match 91.9%; Score 1418; DB 1; Length 298;  
 Best Local Similarity 88.9%; Pred. 3.4e-117;  
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 MTEQAISPAKPLAGIAAIASTKAVPIERVKLLQVQHSKQIAADKYKGIYDCIVR 60  
 DB 1 MGDDALSPDKDFLAGIAAASKTAIVPIERVKLLQVQHSKQISAEKQYKGIIDCVR 60  
 QY 1PKKGGVLSFWRGNLAVIRYEPYQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 DB 61 IPKGGFSLFWRGNLAVIRYEPYQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 QY 121 GAAGATSLCFYYPIDPAPTRLAADVGSKTEREFGGLDCLVKTSGIRGLYQGFSSVS 180  
 DB 121 GAAGATSLCFYYPIDPAPTRLAADVGSKTEREFGGLDCLVKTSGIRGLYQGFSSVS 180  
 QY 181 VGGIITRYAARFGYVDTAKGMLPDKNTHIVSMMIQTVAVGVSYPPDYRRRMM 240  
 DB 181 VGGIITRYAARFGYVDTAKGMLPDKNTHIVSMMIQTVAVGVSYPPDYRRRMM 240  
 QY 241 OSGRKADIMVTGTVDCKRKIFRDEGKAPFKGAMSVLFRGGAFLVLYDELTKVI 298  
 DB 241 OSGRKADIMVTGTVDCKRKIADEGANAFPKGAMSVLFRGGAFLVLYDELTKVI 298  
 RESULT 8  
 ID ADP1 BOVIN STANDARD; PRT; 297 AA.  
 AC P02722;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)  
 DE (Adenine nucleotide translocator 1) (ANT 1).  
 GN SLIC25A4 OR ANT1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=89229093; PubMed=2540808;  
 RA Powell S.J., Medd S.M., Runswick M.U., Walker J.E.;  
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed  
 RT differences in various tissues.";  
 RL Biochemistry 28:866-873(1989).  
 RN  
 RP SEQUENCE.  
 RP MEDLINE=82188267; PubMed=7076130;  
 RA Aguila H., Misra D., Rulicz M., Klingenberg M.;  
 RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart  
 RT mitochondria.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).  
 RN  
 RP SEQUENCE OF 207-297 FROM N.A.  
 RP MEDLINE=86295775; PubMed=3017341;  
 RA Raemussen U.B., Wohlrab H.;  
 RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and

01-OCT-1989 (Rel. 12, Created)  
01-NOV-1990 (Rel. 16, Last sequence update)  
15-SEP-2003 (Rel. 42, Last annotation update)  
ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
SLC25A4 OR ANTI1.  
Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=89236396; PubMed=2541251;  
Corens A.L., Runswick M.J., Walker J.E.;  
"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";  
J. Mol. Biol. 206:261-280(1989).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=89340499; PubMed=2547778;  
Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Makawa M., Shimizu Y., Shimizu N., Wallace D.C.;  
"A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";  
J. Biol. Chem. 264:13398-14004(1989).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE=88041149; PubMed=2823266;  
Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;  
"cDNA sequence of a human skeletal muscle ADP/ATP translocator. Jack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";  
Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).  
[4]  
SEQUENCE FROM N.A.  
TISSUE=Bre;  
MEDLINE=22388257; PubMed=12477932;  
Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschuler R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow R.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marinsina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toishiyuki S., Carninci P., Prange C., Rata S.S., Loguquallo N.A., Peters G.J., Abramson R.D., Mullaly S.J., Roak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Wocley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Rodriguez R.A., Fahey J., Helton B., Kettman M., Madan A., Lu X., Gibbs S.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalls D.E., Schmechel A., Schein U.B., Jones S.U.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[5]  
SEQUENCE OF 1-37 FROM N.A.  
TISSUE=Liver;  
MEDLINE=88124845; PubMed=2829183;  
Houldsworth J., Altardi G.;  
"Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";  
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
[6]  
VARIANTS PRO-114 AND MET-289.  
MEDLINE=20385067; PubMed=10926511;  
Kaakonen J., Jussellius J.K., Tiranli V., Kytälä A., Zeviani M., Comi G.P., Keznen J., Peltonen L., Suomalainen A.;  
"Role of adenine nucleotide translocator 1 in mtDNA maintenance.";  
Science 289:782-785(2000).  
-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant  
 CC progressive external ophthalmoplegia with various mitochondrial  
 CC DNA deletions (PEO). Patients with PEO have mitochondrial  
 CC myopathy, progressive external ophthalmoplegia, and other  
 CC abnormalities associated with multiple different deletions of  
 CC mitochondrial DNA.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 CC DR EMBL; J02966; AAA61223.1; -.  
 CC DR EMBL; J03593; AAA56751.1; -.  
 CC DR EMBL; J04982; AAA51736.1; -.  
 CC DR EMBL; BC008664; AA08664.1; -.  
 CC DR PIR; A44778; A44778.  
 CC DR Genem; HGNC:10990; SLC25A4.  
 CC DR MIM; 103220; -.  
 CC DR MIM; 157640; -.  
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC DR GO; GO:0005739; C:mitochondrion; TAS.  
 CC DR GO; GO:0015207; P:adenine transporter activity; TAS.  
 CC DR GO; GO:0006091; P:energy pathways; TAS.  
 CC DR GO; GO:0006092; P:mitochondrial genome maintenance; TAS.  
 CC DR GO; GO:0006832; P:small molecule transport; TAS.  
 CC DR InterPro; IPR002067; Mtc\_carrier.  
 CC DR InterPro; IPR02030; Mtc\_uncoupling.  
 CC DR Pfam; PF00153; mltc\_carr; 3.  
 CC DR PRINTS; PR00926; MITOCARRIER.  
 CC DR PRINTS; PR00784; MTNCOUPLING.  
 CC DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 CC DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 CC MultiGene family; Disease mutation.  
 CC KW TRANSMEM 12 29 1 (POTENTIAL).  
 CC FT TRANSMEM 73 91 2 (POTENTIAL).  
 CC FT TRANSMEM 117 134 3 (POTENTIAL).  
 CC FT TRANSMEM 176 195 4 (POTENTIAL).  
 CC FT TRANSMEM 214 231 5 (POTENTIAL).  
 CC FT TRANSMEM 273 291 6 (POTENTIAL).  
 CC FT REPEAT 1 110 1.  
 CC FT REPEAT 111 208 2.  
 CC FT REPEAT 209 298 3.  
 CC FT VARIANT 114 114 A->P (IN PEO).  
 CC FT VARIANT 289 289 V->M (IN PEO).  
 CC FT VARIANT 289 289 /FTID=VAR\_012111.  
 CC FT CONFLICT 16 16 G->A (IN REF. 3).  
 CC FT CONFLICT 147 149 KGA->R (IN REF. 3).  
 CC FT CONFLICT 227 227 V->L (IN REF. 3).  
 CC SO SEQUENCE 298 AA; 33064 MW; 59F0DPAEC4E7CFBB CRC64;  
 CC -----  
 CC Query Match 91.3%; Score 1409; DB 1; Length 298;  
 CC Best Local Similarity 88.3%; Pred. No. 2.1e-116;  
 CC Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;  
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 CC QY 1 MTEQASIPAKDPLAGIAAIAIKTAIVAPIERVKLLQVOHASKQIAADKQYGIYDQVR 60  
 CC DB 1 MGDHMSFLKDFLAGVAVAASKTIVAPIERVKLLQVOHASKQIAAEKQYGIIDQVR 60  
 CC QY 1 PKKGVSLSPKRGNIANVIRYPTQALNPAFKDKKQIFLGVDVGHGTQFWREAGNLSG 120  
 CC DB 1 PKKGVSLSPKRGNIANVIRYPTQALNPAFKDKKQIFLGVDVGHGTQFWREAGNLSG 120

QY 121 GAAGATSLCFYVLPDFAFRLAADVGSGTEREERGLDCLVTKTSGDINGLYOGPSVS 180  
 DB 121 GAAGATSLCFYVLPDFAFRLAADVGSGTEREERGLDCLVTKTSGDINGLYOGPSVS 180  
 QY 181 VGGIITVAAAFVGYDTPKGLPDKNTHIVSNMIACTVAVAGVSPPTVRRMM 240  
 DB 181 VGGIITVAAAFVGYDTPKGLPDKNTHIVSNMIACTVAVAGVSPPTVRRMM 240  
 QY 241 QSGRKGADIMYTGVDGCRKIFRDEGKAFKFGKAMSVNLRGKGAFVLYVDELKKVI 298  
 DB 241 QSGRKGADIMYTGVDGCRKIFRDEGKAFKFGKAMSVNLRGKGAFVLYVDELKKVI 298  
 RESULT 10  
 ADT DROME STANDARD; PRT; 299 AA.  
 AC 026365; P91614; Q26254; Q95S30; Q9VZ70;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
 DE translocator) (ANT) (Stress sensitive B protein).  
 GN SEB OR A/A-T OR CG16944.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NX NCBI\_Taxid=7227;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92389367; PubMed=1387687;  
 RA Louvi A., Tsitlik S.G.;  
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila  
 RT melanogaster shows a high degree of similarity with the mammalian  
 RT ADP/ATP translocases".  
 RL J. Mol. Evol. 35:44-50(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94350065; PubMed=7520869;  
 RA Hutter P., Karch F.;  
 RT "Molecular analysis of a candidate gene for the reproductive  
 RT isolation between sibling species of Drosophila".  
 RL Experientia 50:749-762(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Oregon-R;  
 RA Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;  
 RT Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Berkley;  
 MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.B., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., McKlos G.L.G.,  
 RA Abril J.F., Abghyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Chew S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glisdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.B., Kodira G.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
Laekko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,  
Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
Nelson D., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
Palazzolo M., Peterson G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
Reiner K., Remington K., Saunders R.D.C., Scheller F., Shen H.,  
Shue B.C., Sider-Kimios I., Simpson M., Skupski M.P., Smith T.,  
Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C. ;  
"The genome sequence of *Drosophila melanogaster*." ;  
Science 287:2185-2195(2000) .  
[5]  
SEQUENCE FROM N.A.  
RC STRAIN-Berkeley, TISSUE-larva, Ovary, and Pupae;  
RX MEDLINE=22426066; PubMed=12537569;  
RA Stapleton A., Carlson J.W., Brokstein P., Yu C., Champagne M.,  
RA George R.A., Guanin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,  
RA Rubin G.M., Celinker S.B. ;  
RT "A *Drosophila* full-length cDNA resource." ;  
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002)  
CC -I- FUNCTION: Catalyzes the exchange of ADP and ATP across the  
CC mitochondrial inner membrane.  
CC -I- SUBUNIT: Homodimer (By similarity).  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -I- DOMAIN: Composed of three homologous domains.  
CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk) ).  
CC -----  
DR EMBL; S43651; AAB3114.1; -;  
DR EMBL; S71762; AAB31734.3; -;  
DR EMBL; Y10618; CAA71628.1; -;  
DR EMBL; AE003484; AAF47957.1; -;  
DR EMBL; AY060978; AAL28526.1; -;  
DR EMBL; AY070894; AAL48516.1; -;  
DR FLYBase; FBgn003360; se88.  
DR GO; GO:0005743; C:mitochondrial inner membrane; IEP.  
DR GO; GO:0006839; P:mitochondrial transport; IMP.  
DR InterPro; IPR002067; Mit carrier.  
DR InterPro; IPR001993; Mitoch carrier.  
DR Pfam; PF00153; mito\_carr; 2.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH CARRIER; 3.  
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
FT FT TRANSMEM 14 31 1 (POTENTIAL).  
FT TRANSMEM 75 93 2 (POTENTIAL).  
FT TRANSMEM 119 136 3 (POTENTIAL).  
FT TRANSMEM 177 196 4 (POTENTIAL).  
FT TRANSMEM 215 232 5 (POTENTIAL).  
FT TRANSMEM 274 292 6 (POTENTIAL).  
FT CONFLICT 18 19 GI -> QV (IN REF. 1 AND 2).  
FT CONFLICT 81 81 I -> Y (IN REF. 1).  
FT CONFLICT 201 201 MISSING (IN REF. 1 AND 2).  
FT CONFLICT 267 267 TG -> P (IN REF. 1 AND 2).  
FT CONFLICT 268 269 A -> S (IN REF. 1).  
FT CONFLICT 270 270 A -> C (IN REF. 2).  
FT CONFLICT 270 270 A -> C (IN REF. 2).  
SQ SEQUENCE 299 AA; 32909 MW; D51F382AV0BD59B8 CRC64;

Query Match	Best Local Similarity	81.3%	Score 1254.5	DB 1	Length 299
Query Match 237, Conservative	80.6%	Pred. No. 7.5e-103	Matches 237, Conservative	23	Mismatches 33
				Indels 1	Gaps 1
QY	5	AISPAKDFLAGIAAASKTAVAFIEBVKLLQVOHASKQIADKQYKIVDCIARIPE	64		
DB	7	AVGVVQPPAAGGISAASVSKTAVAFIEBVKLLQVOHISKQISPDQYKQKGVNDCTRIPKE	66		
QY	65	QGVLSFWRGNLANVIRIFPTQALNFAFDKTKQIFLGGVDKHTQFWRIFAGNLASGAG	124		
DB	67	QGVSSFWRGKLANVIRIFPTQALNFAFDKTKQYVFLGGVDKHTQFWRIFAGNLASGAG	126		
QY	125	ATSLCPVYPLDPARTRLAADVGSSTERBPRGSDCIWKITKSPGIRGLVQGSFSVYQI	184		
DB	127	ATSLCPVYPLDPARTRLAADVQKGG-QREFTGLNCLTKFKSGIVGLRGSFVSVOGI	185		
QY	185	IITPAAYFGVDTAKGLPDPKNTNIVSWMIAGTVTAVAGVSVPPDYRRRMMOSGR	244		
DB	186	IITPAAYFGVDTAKGLPDPKNTPIIISALQVTTVAGIVSPDYRRRRMMOSGR	245		
QY	245	KGADIMYTGIVDCWRKIIFDEGGKAFPKGAWSNVLRMGAFVLVYDELKVI	298		
DB	246	KATEVITYKNTLHCWATIAKQGGTGAFFKAFNSILRGTGAFVLVYDELKVI	299		
RESULT 11					
ADT-ANOGA		STANDARD;	PRT;	301	AA.
ID	ADT-ANOGA	027238;			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	ADP/ATP carrier protein (ADP/ATP translocase)	(Adenine nucleotide translocator) (ANT)			
OS	Anopheles gambiae (African malaria mosquito).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.				
OX	NCBI_TaxID=7165;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Q3;				
RX	MEDLINE=94348635; PubMed=8069414;				
RA	Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;				
RT	"A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae."				
RL	Insect Mol. Biol. 3:35-40(1994).				
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.				
CC	-1- SUBUNIT: Homodimer (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.				
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.				
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.				
CC	-----				
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CC	EMBL, L11618; AAB04104.1; -				
DR	EMBL, L11617; AAB04105.1; -				
DR	InterPro, IPR002067; Mlt_carrier.				
DR	InterPro, IPR001993; Mitoch_carrier.				
DR	Pfam, PF00153; mltc_carr; 3.				
DR	PRINTS, PR00926; MITOCARRIER.				
DR	PROSITE, PS00215; MITOCH_CARRIER; 3.				
KW	Mitochondion; Inner membrane; Repeat; Transmembrane; Transport.				
FT	TRANSMEM 14 31 1 (POTENTIAL).				
FT	TRANSMEM 75 93 2 (POTENTIAL).				
FT	TRANSMEM 119 136 3 (POTENTIAL).				



Query Match  
Best Local Similarity 77.7%, Pred. No. 2.1e-98;  
Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

Query 1 MTEQA--ISFADFLAGGIAAISTKAVAPIERVLLIQVHASQIADKQKGIIVDCI 58  
Db 1 MTKKADPRGFADPLAGGISAASVSKTAVPIERVLLIQVQASQIADKQKGIIVDCI 60

Query 59 VRIPEQGLSVFRGNLANVIRFPYQALNFAFKDKYKQIFLGVDKHTQFRRYAGNIA 118  
Db 61 VRIPEQGLSVFRGNLANVIRFPYQALNFAFKDKYKQIFLGVDKHTQFRRYAGNIA 120

Query 119 SGGAAGATSLCFVYPLDPAFRTLAADVGSCTEREPRGIDCLVKTISDGIKGIYQGS 178  
Db 121 SGGAAGATSLCFVYPLDPAFRTLAADVGSCTEREPRGIDCLVKTISDGIKGIYQGS 180

Query 179 VSVQGIITIRAYAFGVYDTAKGMLDPPKNTHTIVSWMIAQVTAAGVVSYPFTVRRBM 238  
Db 181 VSVQGIITIRAYAFGVYDTAKGMLDPPKNTHTIVSWMIAQVTAAGVVSYPFTVRRBM 240

Query 239 MMQSGRKADIMYTGTVDCWRKIFRDEGKAFKQAMSNVLRGMGAFLVLYDELKQVI 298  
Db 241 MMQSGRKSEVMYKNTLDQWVKIGKQSGGAFKQAFSNVLRGTGALVLYDEVKALL 300

RESULT 12  
ID ADT\_CHLKE STANDARD; PRT; 339 AA.

AC P31692;  
DT 01-JUN-1993 (Rel. 26, Last sequence update)  
DT 01-JUN-1993 (Rel. 26, Last sequence update)  
DT 15-JUN-1998 (Rel. 36, Last annotation update)  
DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).  
OS Chlorella kessleri.  
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.  
NCBI\_TaxID=3074;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92084708; PubMed=1748677;  
RA Hilgarch C., Sauer N., Tanner W.;  
RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";  
RL J. Biol. Chem. 266:24044-24047(1991).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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CC -----  
CC EMBL, M76669; AAA33027.1; -;  
CC PIR, A41677; A41677.  
CC InterPro, IPR002067; Mlt carrier.  
CC InterPro, IPR001993; Mitoch carrier.  
CC Pfam, PF00153; mltc carr; 3-  
CC PRINTS, PR00936; MITOCARRIER.  
CC PROSITE, PS00215; MITOCH\_CARRIER; 3.

Query Match  
Best Local Similarity 63.4%, Score 978; DB 1; Length 339;  
Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

Query 6 ISFADFLAGGIAAISTKAVAPIERVLLIQVHASQIADK--QKGIIVDCI 63  
Db 39 MAFVLDLAGGTAGASIKTAVAPIERVLLIQVDSNMKISGVPRYATGVNCFVRSS 98

Query 64 EGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDKHTQFRRYAGNIA 123  
Db 99 EGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDKHTQFRRYAGNIA 157

Query 124 GATSLCFVYPLDPAFRTLAADVGSCTEREPRGIDCLVKTISDGIKGIYQGS 183  
Db 158 GATSLCFVYPLDPAFRTLAADVGSCTEREPRGIDCLVKTISDGIKGIYQGS 216

Query 184 IIRAYAFGVYDTAKGMLDPPKNTHTIVSWMIAQVTAAGVVSYPFTVRRBM 242  
Db 217 IIRAYAFGVYDTAKGMLDPPKNTHTIVSWMIAQVTAAGVVSYPFTVRRBM 276

Query 243 GRKADIMYTGTVDCWRKIFRDEGKAFKQAMSNVLRGMGAFLVLYDELKQVI 298  
Db 277 --GGERQYNGTIDQWVKIGKQSGGAFKQAFSNVLRGTGALVLYDEVKALL 329

RESULT 13  
ID ADT3\_YEAST STANDARD; PRT; 307 AA.

AC P16238;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE ADP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).  
GN AACC OR YBR085W OR YBR0753.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90324269; PubMed=2165073;  
RA Kolarov J., Kolarova N., Nelson N.;  
RT "A third ADP/ATP translocator gene in yeast.";  
RL J. Biol. Chem. 265:12711-12716(1990).  
CC [2]  
CC SEQUENCE FROM N.A.  
CC STRAIN=S288c;  
CC Andre B., Cziepluch C., Hein C., Jauniaux J.C., Ureastarazu A.;  
CC Viessers S.;  
CC Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
CC [3]  
CC SEQUENCE OF 38-307 FROM N.A.  
CC Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;  
CC Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC -----



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DR EMBL; M34076; AAA97485.1; -  
DR EMBL; Z35954; CAA85031.1; -  
DR PIR; A36582; A36582.  
DR SGD; S0000289; AAC3.  
DR GO; GO:0005471; F:ATP/ADP antiporter activity; IMP.  
DR GO; GO:0006854; P:ATP/ADP exchange; IMP.  
DR InterPro; IPR002067; Mlt carrier.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mltc\_carr; 3.  
DR PRINTS; PR00926; MITOCHCARRIER.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 2.  
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
KW Multigene family.  
FT TRANSMEM 16 33 1 (POTENTIAL).  
FT TRANSMEM 78 96 2 (POTENTIAL).  
FT TRANSMEM 120 137 3 (POTENTIAL).  
FT TRANSMEM 181 200 4 (POTENTIAL).  
FT TRANSMEM 220 237 5 (POTENTIAL).  
FT TRANSMEM 276 294 6 (POTENTIAL).  
SQ SEQUENCE 307 AA; 33313 MW; D0C1329FEC1BADC8 CRC64;

Query Match 50.5%; Score 778.5; DB 1; Length 307;  
Best Local Similarity 53.7%; Pred. No. 4.5e-61;  
Matches 161; Conservative 45; Mismatches 85; Indels 9; Gaps 5;

QY 3 EQAISPAPDLAGGIAAISTAVAPIRKYLLQVQ-HASKQIADKQYKGIYDQIVRI 61  
DB 7 QOETNFANFLMGVSAIAIAKTAASPIERKILLIONQDEMIKQGTLDKRYGIVDCFRKT 66  
QY 62 PKEGVSLFWRGNTLVNRYRPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASGG 121  
DB 67 AKQEBLSFWRGNTLVNRYRPTQALNFAFKDKIKLMF--GPKKEEGYGMKPAAGNLASGG 124  
QY 122 AAGATSLCFVYPLDFARTLADV--GKSGTERBERGGLDCLVITKSDGIRGLYOGFSV 179  
DB 125 AAGATSLCFVYPLDFARTLADV--GKSGTERBERGGLDCLVITKSDGIRGLYOGFSV 184  
QY 180 SVGGIIIRAAVFGVYDTAKEM-LPDPKNTIIVSWMLAQVTVAAGVSYPPFTVRBM 238  
DB 185 SVGGIIVVRGLYFGVDFSLKPLVLTGSLDGSFLASFLIGVTTGASTCSYPLDVRBM 244  
QY 239 MMQSGRKADIMYGTVDCKRKIFRDEGKAFPGKAMSNVLRMGAGAVVLYLYBELKVI 298  
DB 245 MMTSGQA--VKYNGALDCLKTIASSEGVSILFKGCGANILRSVAGAVISMYDQLQMIT 301

RESULT 14  
ADT\_CHLRE STANDARD; PRT; 308 AA.  
AC P27080;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
translocator) (ANT).  
GN ABT.  
OS Chlamydomonas reinhardtii.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadaceae; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FUD44-R2;  
RX MEDLINE=93204877; PubMed=8455552;  
RA Sharpe J.A., Day A.;

RT "Structure, evolution and expression of the mitochondrial ADP/ATP  
RT translocator gene from Chlamydomonas reinhardtii.",  
RL Mol. Gen. Genet. 237:134-144(1993).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
CC MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; X65194; CAA46311.1; -  
DR PIR; S30259; S30259.  
DR InterPro; IPR002067; Mlt carrier.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mltc\_carr; 3.  
DR PRINTS; PR00926; MITOCHCARRIER.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 2.  
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
FT TRANSMEM 12 29 1 (POTENTIAL).  
FT TRANSMEM 74 92 2 (POTENTIAL).  
FT TRANSMEM 116 133 3 (POTENTIAL).  
FT TRANSMEM 178 197 4 (POTENTIAL).  
FT TRANSMEM 217 234 5 (POTENTIAL).  
FT TRANSMEM 273 291 6 (POTENTIAL).  
SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 50.0%; Score 772; DB 1; Length 308;  
Best Local Similarity 51.8%; Pred. No. 1.7e-60;  
Matches 157; Conservative 55; Mismatches 81; Indels 10; Gaps 5;

QY 1 MTEQAISPAPDLAGGIAAISTAVAPIRKYLLQVQ-HASKQIADKQYKGIYDQIVRI 59  
DB 1 MAKEKKNMVDVFLAGLSAANVSKTAAPPIERVKILLIONQDEMIKQGTLDKRYGIVDCFRKT 60  
QY 60 RIPEQGVLSFWRGNTLVNRYRPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAS 119  
DB 61 RTVEBERGSLMRNTLVNRYRPTQALNFAFKDKIKLMF--GPKKEEGYGMKPAAGNLAS 118  
QY 120 GGAAGATSLCFVYPLDFARTLADV--VGKSGTERBERGGLDCLVITKSDGIRGLYOG 176  
DB 119 GGAAGATSLCFVYPLDFARTLADV--VGKSGTERBERGGLDCLVITKSDGIRGLYOG 178  
QY 177 FSVSVGGIIIRAAVFGVYDTAKM-LPDPKNTIIVSWMLAQVTVAAGVSYPPFTVR 235  
DB 179 FSVSVGGIIIRAAVFGVYDTAKM-LPDPKNTIIVSWMLAQVTVAAGVSYPPFTVR 238  
QY 236 RRMQSGRKADIMYGTVDCKRKIFRDEGKAFPGKAMSNVLRMGAGAVVLYLYBELK 295  
DB 239 RRMQSGRKADIMYGTVDCKRKIFRDEGKAFPGKAMSNVLRMGAGAVVLYLYBELK 295  
QY 296 KVI 298  
DB 296 VIL 298

RESULT 15  
ADT\_SCHPO STANDARD; PRT; 322 AA.  
AC Q09188;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
translocator) (ANT).  
GN ABT.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:34:56 ; Search time 35.2542 Seconds  
(without alignments)  
1337.197 Million cell updates/sec

Title: US-09-811-131-31

Perfect score: 1553  
Sequence: 1 MGHANFLDPLAGAVAA.....LRGNGAFVLVDIKKYV 297

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A Geneseq 19Jun03:\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
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- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1553	100.0	297	21	AAV71031
2	1553	100.0	297	22	AAU01198
3	1553	100.0	297	23	AAU01378
4	1457.5	93.9	298	19	AAU01169
5	1442.5	92.9	293	22	ABU53219
6	1398.5	90.1	298	23	AAO18516
7	1391.5	89.6	298	21	AAV71032
8	1391.5	89.6	298	22	AAU01199
9	1391.5	89.6	298	23	AAU01379

10	1385.5	89.2	298	21	AAV71033	Human adenine nucl
11	1385.5	89.2	298	22	AAU39641	Human polypeptide
12	1385.5	89.2	298	22	AAU01200	Human adenine nucl
13	1385.5	89.2	298	23	AAU01380	Human adenine nucl
14	1385.5	89.2	323	22	AAU41427	Human polypeptide
15	1294.5	83.4	325	22	ABG15423	Novel human diageno
16	1268.5	81.7	429	24	ABR41715	Human DTRP organe
17	1241	79.9	299	22	ABR66082	Drosophila melanog
18	1241	79.9	299	22	ABR67200	Drosophila melanog
19	1221.5	78.7	263	22	ABR7056	Novel human diageno
20	1147	73.9	307	22	ABR58380	Drosophila melanog
21	1101.5	70.9	315	22	ABU53218	Human metabolism-a
22	1101.5	70.9	315	23	AAK21175	Human TRICH-19 pro
23	926.5	59.7	228	23	ABP43205	Human ovarian anti
24	867.5	55.9	222	23	ABP74106	Human TRICH SEQ ID
25	820	52.8	298	22	ABG18922	Novel human diageno
26	771	49.6	301	23	ABP13357	Candida albicans e
27	746.5	48.1	379	24	ABR81267	Arabidopsis thalia
28	746	48.0	346	21	AAK36577	Arabidopsis thalia
29	746	48.0	346	21	AAK37261	Arabidopsis thalia
30	746	48.0	346	21	AAK37264	Arabidopsis thalia
31	746	48.0	346	21	AAK38460	Arabidopsis thalia
32	746	48.0	363	21	AAK36576	Arabidopsis thalia
33	746	48.0	363	21	AAK37260	Arabidopsis thalia
34	746	48.0	363	21	AAK37263	Arabidopsis thalia
35	746	48.0	363	21	AAK38459	Arabidopsis thalia
36	746	48.0	381	21	AAK36575	Arabidopsis thalia
37	746	48.0	381	21	AAK37259	Arabidopsis thalia
38	746	48.0	381	21	AAK37262	Arabidopsis thalia
39	746	48.0	381	21	AAK38458	Arabidopsis thalia
40	746	48.0	992	21	AAK38672	Arabidopsis thalia
41	746	48.0	1009	21	AAK38671	Arabidopsis thalia
42	746	48.0	1027	21	AAK38670	Arabidopsis thalia
43	743	47.8	346	21	AAK17731	Arabidopsis thalia
44	743	47.8	363	21	AAK17730	Arabidopsis thalia
45	743	47.8	381	21	AAK17729	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1	AAV71031	standard; Protein; 297 AA.
ID	AAV71031	
AC	AAV71031	
XX		
DT	29-AUG-2000	(first entry)
XX		
DE	Human adenine nucleotide translocator ANTI.	
XX		
KW	Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;	
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;	
KW	mitochondrial permeability transition; neuroprotective; nocitropic;	
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW	antiparkinsonic; cerebroprotective; therapeutic; screening; psoriasis;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;	
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;	
KW	myoclonic epilepsy red ragged fibre syndrome.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200026370-A2.	
XX		
PD	11-MAY-2000.	
XX		
PF	03-NOV-1999;	99WO-US25883.
XX		
PR	03-NOV-1998;	98US-0185904.
PR	08-SEP-1999;	99US-0393441.
XX		

PA (MITO-) MITOKOR.  
 XX  
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,  
 PI Ghosh SS;  
 XX  
 XX WPI, 2000-365619/31.  
 DR N-PSDB; AAD00519.  
 XX  
 XX Recombinant construct encoding adenine nucleotide translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease -  
 XX  
 XX Claim 44, Page 172, 175pp; English.  
 XX  
 XX The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MTDD) and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT1 from human brain.  
 XX  
 XX Sequence 297 AA;  
 SQ  
 Query Match 100.0%; Score 1553; DB 21; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;  
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIEVKLLQVQHASKOISAEKQYKGIIDCVVR 60  
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIEVKLLQVQHASKOISAEKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGKMLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQFWRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGKMLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYPLDFAFTRLAADVGRRAQREFFGLDCCIIRKPSDGLRGLYGFNVSV 180  
 DB 121 GAAGATSLCFYPLDFAFTRLAADVGRRAQREFFGLDCCIIRKPSDGLRGLYGFNVSV 180  
 QY 181 QGIIYRAAYGVVDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSYFPDTRRRMMQ 240  
 DB 181 QGIIYRAAYGVVDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSYFPDTRRRMMQ 240  
 QY 241 SGRKADIMYGTVDCKRKIAKBGAKAFPGKAMSVNLRGMGAFVLYLDEIKKYV 297  
 DB 241 SGRKADIMYGTVDCKRKIAKBGAKAFPGKAMSVNLRGMGAFVLYLDEIKKYV 297

RESULT 2  
 AAU01198  
 ID AAU01198 standard; Protein; 297 AA.  
 AC AAU01198;  
 XX  
 XX 07-SEP-2001 (first entry)  
 XX  
 XX Human adenine nucleotide translocator-1 (ANT-1) protein.  
 DE Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;  
 XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX  
 OS Homo sapiens.  
 XX  
 XX WO200132876-A2.  
 PN  
 XX  
 XX 10-MAY-2001.  
 PD  
 XX  
 XX 03-NOV-2000; 2000WO-US30535.  
 PF  
 XX  
 XX 03-NOV-1999; 99US-0434354.  
 PR  
 XX  
 XX (MITO-) MITOKOR.  
 PA  
 XX  
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritger LG;  
 PI Veljiceleb G, Davis RE;  
 XX  
 XX WPI, 2001-291054/30.  
 DR N-PSDB; AAS05901.  
 DR  
 XX  
 XX New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 XX  
 XX Disclosure; Fig 2; 186pp; English.  
 PS  
 XX  
 XX The present sequence represents human adenine nucleotide translocator-1  
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability  
 CC transition (MPT) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.  
 XX  
 XX Sequence 297 AA;  
 SQ  
 Query Match 100.0%; Score 1553; DB 22; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;  
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIEVKLLQVQHASKOISAEKQYKGIIDCVVR 60  
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIEVKLLQVQHASKOISAEKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGKMLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQFWRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGKMLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYPLDFAFTRLAADVGRRAQREFFGLDCCIIRKPSDGLRGLYGFNVSV 180  
 DB 121 GAAGATSLCFYPLDFAFTRLAADVGRRAQREFFGLDCCIIRKPSDGLRGLYGFNVSV 180  
 QY 181 QGIIYRAAYGVVDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSYFPDTRRRMMQ 240  
 DB 181 QGIIYRAAYGVVDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSYFPDTRRRMMQ 240  
 QY 241 SGRKADIMYGTVDCKRKIAKBGAKAFPGKAMSVNLRGMGAFVLYLDEIKKYV 297  
 DB 241 SGRKADIMYGTVDCKRKIAKBGAKAFPGKAMSVNLRGMGAFVLYLDEIKKYV 297

## RESULT 3

AAU10378

ID AAN10378 standard; Protein; 297 AA.

XX AAU10378;

XX 14-FEB-2002 (first entry)

XX Human adenine nucleotide translocator 1 (ANT1).

XX Human; adenine nucleotide translocator; ANT1;

XX mitochondrial matrix protein.

XX Homo sapiens.

XX MO200185944-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001WO-US15416.

XX 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;

XX Ghosh SS, Moos WH, Pei Y, Carroll AK;

XX WPI; 2002-055598/07.

XX N-PSDB; AAS16688.

XX Claim 44; Fig 2; 147p; English.

XX The invention relates to a recombinant expression construct (I)

XX comprising a regulated promoter operably linked to a nucleic acid

XX encoding an adenine nucleotide translocator (ANT) polypeptide. ANT

XX proteins mediate the exchange of ATP synthesized in the mitochondrial

XX matrix for ADP in the cytosol. (I) is useful for producing recombinant

XX ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and

XX culturing the host cell. (I) is also useful for targeting a polypeptide

XX of interest to a mitochondrial membrane, where ANT polypeptide is

XX expressed as a fusion protein with the polypeptide of interest.

XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is

XX useful for identifying an agent that binds to an ANT polypeptide. ANT

XX ligand is useful for determining the presence of an ANT polypeptide.

XX preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating

XX ANT from a biological sample, where the ANT ligand is covalently or non-

XX covalently bound to a solid phase. Detectably labeled ANT ligand is also

XX useful for identifying an agent that interacts with an ANT polypeptide.

XX The present sequence represents the amino acid sequence of human ANT1.

XX

XX

SQ Sequence 297 AA;

Query Match 100.0%; Score 1553; DB 23; Length 297;

Best Local Similarity 100.0%; Pred. No. 3,4e-173;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHAWSLKDFLAGAANAASVKTAVPIERVKLLQVQASAKQISAEKYKGIIDCVNR 60

DB 1 MGDHAWSLKDFLAGAANAASVKTAVPIERVKLLQVQASAKQISAEKYKGIIDCVNR 60

QY 61 IPKEGFTLFWRGVLANVIRYPTQALNFAFKDKKQFLGCVNRHKKQFMYYPAGNLASG 120

DB 61 IPKEGFTLFWRGVLANVIRYPTQALNFAFKDKKQFLGCVNRHKKQFMYYPAGNLASG 120

QY 121 GAAGATSCFYVPLDFAFTRILADVGRRARQREFFGLGDCIIRKPSDGLRGLYGFNVSV 180

DB 121 GAAGATSCFYVPLDFAFTRILADVGRRARQREFFGLGDCIIRKPSDGLRGLYGFNVSV 180

QY 181 QGIIYRAAYFGVYDTAKGLPDPKQVHIFVSWMIASQVTAVALSLYPTDVRBRMMQ 240

DB 181 QGIIYRAAYFGVYDTAKGLPDPKQVHIFVSWMIASQVTAVALSLYPTDVRBRMMQ 240

QY 241 SGRKADIMYTGTVDCWRKIAKDEGAAVFKGASVNLRGGAFLVLYDEIRKVV 297

DB 241 SGRKADIMYTGTVDCWRKIAKDEGAAVFKGASVNLRGGAFLVLYDEIRKVV 297

## RESULT 4

AAM61169

ID AAM61169 standard; Protein; 298 AA.

XX AAM61169;

XX 28-SEP-1998 (first entry)

XX Ant1 protein.

XX Ant1; Adenine nucleotide translocator; cloning; screening;

XX DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;

XX probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;

XX hypertrophic cardiomyopathy; fasciocalcular humeral muscular dystrophy;

XX lactic acidosis; degenerative muscle disease.

XX Mus sp.

XX WO9819714-A1.

XX 14-MAY-1998.

XX 31-OCT-1997; 97WO-US19882.

XX 01-NOV-1996; 96US-0030017.

XX (UYEM-) UNIV EMORY.

XX Graham BC, Macgregor GR, Wallace DC;

XX WPI; 1998-286608/25.

XX N-PSDB; AAV36479.

XX Disclosure; Page 39-40; 61p; English.

XX The present sequence is the mouse Ant1 protein, the cDNA producing this

XX polypeptide is cloned by screening a mouse heart cDNA library with the

XX human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA

XX Tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by

XX the Ant1 locus, a nuclear gene on chromosome 8. This protein is required

XX in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP

XX which can then be converted into ATP. An Ant1 homozygous mutant would

XX thus be defective in OXPHOS which results in disease in oxidative

XX metabolism dependent tissues. This mouse Ant1 homozygous mutant can be

XX used as a model system for fasciocalcular humeral muscular dystrophy,

XX hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model

XX systems can be used to test possible therapeutic compounds which

XX increase/mediate ATP and ADP exchange across the mitochondrial membrane

XX independent of ANT1.

SQ Sequence 298 AA;

Query Match 93.9%; Score 1457.5; DB 19; Length 298;

Best Local Similarity 93.6%; Pred. No. 5,4e-162;

Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 MGDHAWSLKDFLAGAANAASVKTAVPIERVKLLQVQASAKQISAEKYKGIIDCVNR 60

DB 1 MGDHAWSLKDFLAGAANAASVKTAVPIERVKLLQVQASAKQISAEKYKGIIDCVNR 60

QY 61 IPEKGFSLSPKGNLANVIRYPTALNPAFDKTKOLFLGSDVDRHKQFWRFEAGNLASG 120  
DB 61 IPEKGFSLSPKGNLANVIRYPTALNPAFDKTKOLFLGSDVDRHKQFWRFEAGNLASG 120  
QY 121 GAAGTSLCFVYPLDPAFTRTLADVGR-RAOREFPGLDGCIKIKRSGDLRGLYOGFNVSGI 179  
DB 121 GAAGTSLCFVYPLDPAFTRTLADVGR-RAOREFPGLDGCIKIKRSGDLRGLYOGFNVSGI 180  
QY 180 VOGIIIVRAAFVGVYDTAKGMLPDPKXVHIIVSNMIAOSVTAVAGLSTYPTVRRMMQSGR 239  
DB 181 VOGIIIVRAAFVGVYDTAKGMLPDPKXVHIIVSNMIAOSVTAVAGLSTYPTVRRMMQSGR 240  
QY 240 QSGRKGADIMYTGTLDCWRKTLAKDEGAKAFPGKANSNVLRGKGAFLVLYDEIKKY 297  
DB 241 QSGRKGADIMYTGTLDCWRKTLAKDEGAKAFPGKANSNVLRGKGAFLVLYDEIKKY 298

## RESULT 5

ABUS3219  
ID ABUS3219 standard; Protein; 293 AA.

AC ABUS3219;  
XX  
DT 14-APR-2003 (first entry)  
XX  
DE Human metabolism-associated DKFZphtest\_35n12 homologue #1.  
XX  
KW Human; gene therapy; vaccine; disease treatment; detection.  
XX  
OS Homo sapiens.  
XX  
PN WO200112659-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 18-AUG-2000; 2000WO-B01496.  
XX  
PR 18-AUG-1999; 99US-0149499.  
XX  
PR 28-SEP-1999; 99US-0156503.  
XX  
PA (GHEU-) GERMAN HUMAN GENOME PROJECT.  
XX  
PI Wiemann S;  
XX  
DR WPI; 2001-327840/34.  
XX  
PT Nucleic acids having the sequences of clones isolated from libraries of  
XX different human tissues, useful in recombinant DNA methodologies -  
XX  
PS Example III; Page 850; 1095pp; English.  
XX  
CC This invention describes novel polynucleotides and polypeptides isolated  
XX from human cDNA libraries which can be used for gene therapy or in  
XX vaccines. The polynucleotides of the invention and antibodies encoded by  
XX them may be used in the prevention, diagnosis and treatment of diseases  
XX associated with inappropriate polypeptide expression. The products of the  
XX invention may also be used to identify modulators of expression and  
XX activity and to down regulate expression and activity. The antibodies of  
XX the invention may also be used as diagnostic agents for detecting the  
XX presence of polypeptides in samples. This sequence represents a homologue  
XX of a polypeptide described in the disclosure of the invention.  
XX  
SQ Sequence 293 AA;

Query Match 92.9%; Score 1442.5; DB 22; Length 293;  
Best Local Similarity 94.2%; Fred. No. 3e-160;  
Matches 276; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 5 AMSFLKDFLAGVAANAASKTAAVAFIERVTLLOVQHASQVIAEKQYKGIIDCVRIPIKE 64  
DB 1 AHSFLKDFLAGGIAAASKTAAVAFIERVTLLOVQHASQVIAEKQYKGIIDCVRIPIKE 60

QY 65 QGFLSPKGNLANVIRYPTALNPAFDKTKOLFLGSDVDRHKQFWRFEAGNLASGGAAG 124  
DB 61 QGFLSPKGNLANVIRYPTALNPAFDKTKOLFLGSDVDRHKQFWRFEAGNLASGGAAG 120  
QY 125 ATSLCFVYPLDPAFTRTLADVGR-RAOREFPGLDGCIKIKRSGDLRGLYOGFNVSGI 183  
DB 121 ATSLCFVYPLDPAFTRTLADVGR-RAOREFPGLDGCIKIKRSGDLRGLYOGFNVSGI 180  
QY 184 IIVRAAFVGVYDTAKGMLPDPKXVHIIVSNMIAOSVTAVAGLSTYPTVRRMMQSGR 243  
DB 181 IIVRAAFVGVYDTAKGMLPDPKXVHIIVSNMIAOSVTAVAGLSTYPTVRRMMQSGR 240  
QY 244 KGADIMYTGTLDCWRKTLAKDEGAKAFPGKANSNVLRGKGAFLVLYDEIKKY 296  
DB 241 KGADIMYTGTLDCWRKTLAKDEGAKAFPGKANSNVLRGKGAFLVLYDEIKKY 293

## RESULT 6

AA018516  
ID AA018516 standard; Protein; 298 AA.

AC AA018516;  
XX  
DT 11-OCT-2002 (first entry)  
XX  
DE Human insulin receptor signaling modifier SEQ ID NO: 54.  
XX  
KW Human; insulin receptor signaling; insulin receptor signaling modifier;  
XX ISM; diabetes; metabolic syndrome; antidiabetic.  
XX  
OS Homo sapiens.  
XX  
PN WO200255664-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 11-JAN-2002; 2002WO-US01048.  
XX  
PR 12-JAN-2001; 2001US-261226P.  
XX  
PR 12-JAN-2001; 2001US-261303P.  
XX  
PR 12-JAN-2001; 2001US-261304P.  
XX  
PR 12-JAN-2001; 2001US-261335P.  
XX  
PR 12-JAN-2001; 2001US-261361P.  
XX  
PR 12-JAN-2001; 2001US-261362P.  
XX  
PR 12-JAN-2001; 2001US-261456P.  
XX  
PR 12-JAN-2001; 2001US-261457P.  
XX  
PR 12-JAN-2001; 2001US-261458P.  
XX  
PR 12-JAN-2001; 2001US-261459P.  
XX  
PR 12-JAN-2001; 2001US-261461P.  
XX  
PR 12-JAN-2001; 2001US-261518P.  
XX  
PR 12-JAN-2001; 2001US-261531P.  
XX  
PR 12-JAN-2001; 2001US-261532P.  
XX  
PR 12-JAN-2001; 2001US-261589P.  
XX  
PR 12-JAN-2001; 2001US-261590P.  
XX  
PR 12-JAN-2001; 2001US-261694P.  
XX  
PR 12-JAN-2001; 2001US-261695P.  
XX  
PR 12-JAN-2001; 2001US-261697P.

(EXEL-) EXELIXIS INC.

PI Seidel-Dugan C, Ferguson KC, Kidd T;  
XX  
DR WPI; 2002-599664/64.  
XX  
DR N-PSDB; AAL48635.  
XX

PT Identifying an insulin receptor signaling modulator, useful as drug  
PT targets for treating diabetes or metabolic disorders, comprises  
PT contacting an assay system comprising insulin receptor signaling  
PT modifiers with a test agent -  
XX  
PS Disclosure; Page 160-161; 232pp; English.  
XX  
CC The present invention relates to a method of identifying a candidate

CC insulin receptor (INR) signaling modulating agent, involving contacting  
CC an assay system comprising an insulin receptor signaling modifier (ISM)  
CC polypeptide or nucleic acid with a test agent, and detecting a test  
CC agent-biased activity of the assay system. The method is useful for  
CC identifying candidate INR signaling modulating agents. ISM genes may be  
CC used as drug targets for treatment of disorders related to INR signaling  
CC such as diabetes or metabolic syndrome. ISM nucleic acids and  
CC polypeptides are useful for identifying and testing agents that modulate  
CC ISM function and for other applications related to the involvement of ISM  
CC in INR signaling, and for identifying subjects having a predisposition to  
CC such diseases associated with INR signaling. The present sequence is an  
CC ISM protein described in the exemplification of the invention.

XX Sequence 298 AA;

Query Match 90.1%; Score 1398.5; DB 23; Length 298;  
Best Local Similarity 88.9%; Pred. No. 4.5e-155;  
Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MGDHAFSLDPLAGVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVNR 60  
DB 1 MTDAAVSPADPLAGVAAVSKTAVAPIERVKLLQVQHASKOITADKQYGIIDCVNR 60  
QY 61 IPKEQGLSPFWRGNLANVIRYPTQALNPAFKDKYKQLFLGVDVRHQPFRYFAGNLASG 120  
DB 61 IPKEQGLSPFWRGNLANVIRYPTQALNPAFKDKYKQLFLGVDVRHQPFRYFAGNLASG 120  
QY 121 GAAGATSLCFVYPLDPAFRTLADVGR-AQREPHIGDCTIKIKPSDGLRGILYQGFNV 179  
DB 121 GAAGATSLCFVYPLDPAFRTLADVGR-AQREPHIGDCTIKIKPSDGLRGILYQGFNV 180  
QY 180 VQGIITRAAYFGVYDPAKGM-LDPKRVHIFVSMNIOSTYAVAGLSYFPDVRMM 239  
DB 181 VQGIITRAAYFGVYDPAKGM-LDPKRVHIFVSMNIOSTYAVAGLSYFPDVRMM 240  
QY 240 QSGRKGADIMYTGVDCKRIKADGAKAFPGKAMSVNLRGMGAFVLVYDEIKKY 296  
DB 241 QSGRKGADIMYTGVDCKRIKADGAKAFPGKAMSVNLRGMGAFVLVYDEIKKY 297

RESULT 7  
AAV71032  
ID AAV71032 standard; Protein; 298 AA.

XX AAV71032;

DT 29-AUG-2000 (first entry)

DE Human adenine nucleotide translocator ANT2.

XX Human, adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;  
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
KW mitochondrial permeability transition; neuroprotective; neurologic;  
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
KW antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.

OS WO200026370-A2.

PN 11-MAY-2000.

PD 03-NOV-1999; 99WO-US25883.

PR 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
PI Ghosh SS;  
XX WPI; 2000-365619/31.  
DR N-PSDB; AAD00520.  
XX Recombinant construct encoding adenine nucleotide translocator  
PT polypeptide, useful e.g. in screening for potential therapeutic agents  
PT against mitochondrial disease  
XX Claim 45; Page 172-173; 175pp; English.

CC The patent discloses a method to produce adenine nucleotide translocator  
CC (ANT) proteins or ANT fusion proteins using recombinant expression  
CC constructs. ANT is a nuclear encoded protein and a major component of  
CC inner mitochondrial membrane. It mediates transport of adenosine  
CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
CC as an important molecular component of the mitochondrial permeability  
CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
CC or ligands that bind to, or interact with it. The ANT ligands are used to  
CC detect or isolate ANT in a biological sample, and therapeutically for  
CC regulating mitochondrial pore activity, for treating diseases associated  
CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondria  
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
CC epilepsy red ragged fibre syndrome. The present sequence is an  
CC adenine nucleotide translocator ANT2 from human brain.

XX Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 21; Length 298;  
Best Local Similarity 88.6%; Pred. No. 3e-154;  
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAFSLDPLAGVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVNR 60  
DB 1 MTDAAVSPADPLAGVAAVSKTAVAPIERVKLLQVQHASKOITADKQYGIIDCVNR 60  
QY 61 IPKEQGLSPFWRGNLANVIRYPTQALNPAFKDKYKQLFLGVDVRHQPFRYFAGNLASG 120  
DB 61 IPKEQGLSPFWRGNLANVIRYPTQALNPAFKDKYKQLFLGVDVRHQPFRYFAGNLASG 120  
QY 121 GAAGATSLCFVYPLDPAFRTLADVGR-AQREPHIGDCTIKIKPSDGLRGILYQGFNV 179  
DB 121 GAAGATSLCFVYPLDPAFRTLADVGR-AQREPHIGDCTIKIKPSDGLRGILYQGFNV 180  
QY 180 VQGIITRAAYFGVYDPAKGM-LDPKRVHIFVSMNIOSTYAVAGLSYFPDVRMM 239  
DB 181 VQGIITRAAYFGVYDPAKGM-LDPKRVHIFVSMNIOSTYAVAGLSYFPDVRMM 240  
QY 240 QSGRKGADIMYTGVDCKRIKADGAKAFPGKAMSVNLRGMGAFVLVYDEIKKY 296  
DB 241 QSGRKGADIMYTGVDCKRIKADGAKAFPGKAMSVNLRGMGAFVLVYDEIKKY 297

RESULT 8  
AAU01199  
ID AAU01199 standard; Protein; 298 AA.

XX AAU01199;

DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-2 (ANT-2) protein.

XX Human, adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;  
KW mitochondrial permeability transition pore component; cell survival;  
KW mitochondrial core component; mitochondrial related disorder; cancer;  
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.



OS Homo sapiens.  
 XX WO200132876-A2.  
 XX 10-MAY-2001.  
 PD 03-NOV-2000; 2000WO-US30535.  
 XX 03-NOV-1999; 99US-0434354.  
 PR (MITO-) MITOKOR.  
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigert LG;  
 PI Velicetebel G, Davis RE;  
 DR N-PSDB; AAS05902.  
 XX WPI; 2001-291054/30.  
 PT New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 XX  
 PS Disclosure: Fig 2; 186pp; English.  
 XX The present sequence represents human adenine nucleotide translocator-2  
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability  
 CC transition (MPT) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLASe sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.  
 CC  
 SQ Sequence 298 AA;  
 Query Match 89.6%; Score 1391.5; DB 22; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 3e-154;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVNR 60  
 DB 1 MTDAALSPAKDFLAGAANAASKTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVNR 60  
 QY 61 IPKEQGFSPFRGNLANVIRFPPTQALNFAFKDKYKQFLGCVDRHKGQFWRYFAGNLSG 120  
 DB 61 IPKEQGVLSFPRGNLANVIRFPPTQALNFAFKDKYKQFLGCVDRHKGQFWRYFAGNLSG 120  
 QY 121 GAAGATSLCFYYPPLDPFARTRLAADVGR- AOREBFGJLDCIIRKPSGDLGGLYOGGFNV 179  
 DB 121 GAAGATSLCFYYPPLDPFARTRLAADVGR- AOREBFGJLDCIIRKPSGDLGGLYOGGFNV 180  
 QY 180 VQGIITRAAYFGVYDTRAKMLPDPKXVHIFVSMIAOSVTAAGLSTYPPDYRRRMM 239  
 DB 181 VQGIITRAAYFGVYDTRAKMLPDPKXVHIFVSMIAOSVTAAGLSTYPPDYRRRMM 240  
 QY 240 OSGRKADIMTGTGDCRKTAKDEGAAFFKGAANSVLKMGCAFVLYLDEIKKY 296  
 DB 241 OSGRKADIMTGTGDCRKTAKDEGAAFFKGAANSVLKMGCAFVLYLDEIKKY 297

AAU10379  
 ID AAU10379 standard; Protein; 298 AA.  
 XX  
 AC AAU10379;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human adenine nucleotide translocator 2 (ANT2).  
 XX Human; adenine nucleotide translocator; ANT; ss;  
 KW mitochondrial matrix protein.  
 XX  
 OS Homo sapiens.  
 XX WO200185944-A2.  
 XX 15-NOV-2001.  
 PD 11-MAY-2001; 2001WO-US15416.  
 XX 11-MAY-2000; 2000US-0569327.  
 PR (MITO-) MITOKOR.  
 XX  
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;  
 DR WPI; 2002-055598/07.  
 DR N-PSDB; AAS16689.  
 XX Novel recombinant expression construct for producing adenine nucleotide  
 PT translocator polypeptides, comprises a regulated promoter linked to  
 PT nucleic acid encoding the polypeptide -  
 XX  
 PS Claim 44; Fig 2; 147pp; English.  
 XX The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT2.  
 CC  
 SQ Sequence 298 AA;  
 Query Match 89.6%; Score 1391.5; DB 23; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 3e-154;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVNR 60  
 DB 1 MTDAALSPAKDFLAGAANAASKTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVNR 60  
 QY 61 IPKEQGFSPFRGNLANVIRFPPTQALNFAFKDKYKQFLGCVDRHKGQFWRYFAGNLSG 120  
 DB 61 IPKEQGVLSFPRGNLANVIRFPPTQALNFAFKDKYKQFLGCVDRHKGQFWRYFAGNLSG 120  
 QY 121 GAAGATSLCFYYPPLDPFARTRLAADVGR- AOREBFGJLDCIIRKPSGDLGGLYOGGFNV 179  
 DB 121 GAAGATSLCFYYPPLDPFARTRLAADVGR- AOREBFGJLDCIIRKPSGDLGGLYOGGFNV 180  
 QY 180 VQGIITRAAYFGVYDTRAKMLPDPKXVHIFVSMIAOSVTAAGLSTYPPDYRRRMM 239

Db 181 VGGIIRAAVFGYVDTAKGMLPDKNTHIVSMIAQVTAVAGVTSYPTDVRRRMM 240  
 QY 240 QSGRKADIMVTGTVDCMRKIADDEGAKAFPKGAMSVNLRGMGAFVLVYDEIKKY 296  
 Db 241 QSGRKADIMVTGTVDCMRKIADDEGAKAFPKGAMSVNLRGMGAFVLVYDEIKKY 297

RESULT 10  
 ID AAY71033 standard; Protein, 298 AA.  
 AC AAY71033;  
 XX 29-AUG-2000 (first entry)  
 DE Human adenine nucleotide translocator ANT3.  
 XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;  
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
 KW mitochondrial permeability transition; neuroprotective; neurotropic;  
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
 KW antiparkinsonian; cerebroprotective; therapeutic; screening; peoriolysis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
 KW myoclonic epilepsy red ragged fibre syndrome.  
 XX Homo sapiens.  
 OS WO200026370-A2.  
 XX 11-MAY-2000.  
 XX 03-NOV-1999; 99WO-US25883.  
 XX 03-NOV-1998; 98US-0185904.  
 PR 08-SEP-1999; 99US-0393441.  
 XX (MITO-) MITOKOR.  
 PA Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS;  
 XX WPI; 2000-365619/31.  
 DR N-PSDB; AAD00521.  
 PT Recombinant construct encoding adenine nucleotide translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease -  
 PS Claim 46; Page 173-174; 175pp; English.  
 XX The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression of  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, peoriolysis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT3 from human brain.  
 XX Sequence 298 AA;  
 XX

Query Match 89.2%; Score 1385.5; DB 21; Length 298;  
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAFSLKDFLAGAANAASKTAVAPISRVKLLQVONASKOISAEKOYKGIIDCVR 60  
 Db 1 MTBQALISFADPFLAGGIAAASKTAVAPISRVKLLQVONASKOIADKQKGVDCIVR 60  
 QY 61 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQLFJGCVDRHKQFMRYPAGNLSG 120  
 Db 61 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQIFJGCVDRHKQFMRYPAGNLSG 120  
 QY 121 GAAGATSLCFVYPLDFPRTLLADVGR-AGREHFGDGLCIKFKSDGRLGYOGFNVS 179  
 Db 121 GAAGATSLCFVYPLDFPRTLLADVGRSGTEREFGADGLVTKSDGRLGYOGFNVS 180  
 QY 180 VGGIIRAAVFGYVDTAKGMLPDKNTHIVSMIAQVTAVAGVTSYPTDVRRRMM 239  
 Db 181 VGGIIRAAVFGYVDTAKGMLPDKNTHIVSMIAQVTAVAGVTSYPTDVRRRMM 240  
 QY 240 QSGRKADIMVTGTVDCMRKIADDEGAKAFPKGAMSVNLRGMGAFVLVYDEIKKY 297  
 Db 241 QSGRKADIMVTGTVDCMRKIADDEGAKAFPKGAMSVNLRGMGAFVLVYDEIKKY 298

RESULT 11  
 ID AAM39641 standard; Protein, 298 AA.  
 AC AAM39641;  
 XX 22-OCT-2001 (first entry)  
 DE Human polypeptide SEQ ID NO 2786.  
 XX Human; neurotropic; immunosuppressant; cytosolic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX Homo sapiens.  
 OS WO200153312-A1.  
 XX 26-JUL-2001.  
 PR 26-DEC-2000; 2000WO-US34263.  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 PA (HSE-) HSEB INC.  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AAI58797.  
 XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX Example 4; SEQ ID NO 2786; 10078bp; English.  
 XX

XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AA158642-AA1642213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

XX Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 22; Length 298;  
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
 DB 1 MTEQAIISPAKDFLAGGIAAIAISKTAVPARERKLLQVQHASKOIAADKQYKGIIDCVR 60  
 QY 61 IPKEQGLSPFRGNLANVIRYPTQALNPAFKDKYKOLFLGVDVHKKQFMRYFAGNLASG 120  
 DB 61 IPKEQGLSPFRGNLANVIRYPTQALNPAFKDKYKOLFLGVDVHKKQFMRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGR-AQREPHGLGDCIIRKPKSDGLRGLYOGFNVS 179  
 DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AQREPHGLGDCIIRKPKSDGLRGLYOGFNVS 180  
 QY 180 VGGIITVRAAYFGVYDTAKGMLPDPKKNVHIFVSMWIAQSVTAVALLSYPPDTRRRMM 239  
 DB 181 VGGIITVRAAYFGVYDTAKGMLPDPKKNVHIFVSMWIAQSVTAVALLSYPPDTRRRMM 240  
 QY 240 QSGRGADIMYTGVDWCWKRIAKDEGAKAFPGKAMSNVLRGMAFVLVYDEIKCYV 297  
 DB 241 QSGRGADIMYTGVDWCWKRIAKDEGAKAFPGKAMSNVLRGMAFVLVYDEIKCYV 298

RESULT 12

AAU01200  
 ID AAU01200 standard; Protein; 298 AA.

XX AAU01200;  
 AC  
 XX  
 DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-3 (ANT-3) protein.

XX Human, adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX Homo sapiens.

XX WO200132876-A2.

XX 10-MAY-2001.

XX 03-NOV-2000; 2000WO-US30535.

XX 03-NOV-1999; 99US-0434354.

XX (MITO-) MITOKOR.

XX Murphy AN, Cleverger W, Wiley SE, Andreyev AY, Frigeri LG;

PI Velicelaeb1 G, Davis RE;

XX WPI; 2001-291054/30.

XX N-PSDB; AA505903.

XX New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -

XX Disclosure; Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-3  
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability  
 CC transition (MPT) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLAHS sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 22; Length 298;  
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
 DB 1 MTEQAIISPAKDFLAGGIAAIAISKTAVPARERKLLQVQHASKOIAADKQYKGIIDCVR 60  
 QY 61 IPKEQGLSPFRGNLANVIRYPTQALNPAFKDKYKOLFLGVDVHKKQFMRYFAGNLASG 120  
 DB 61 IPKEQGLSPFRGNLANVIRYPTQALNPAFKDKYKOLFLGVDVHKKQFMRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGR-AQREPHGLGDCIIRKPKSDGLRGLYOGFNVS 179  
 DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AQREPHGLGDCIIRKPKSDGLRGLYOGFNVS 180  
 QY 180 VGGIITVRAAYFGVYDTAKGMLPDPKKNVHIFVSMWIAQSVTAVALLSYPPDTRRRMM 239  
 DB 181 VGGIITVRAAYFGVYDTAKGMLPDPKKNVHIFVSMWIAQSVTAVALLSYPPDTRRRMM 240  
 QY 240 QSGRGADIMYTGVDWCWKRIAKDEGAKAFPGKAMSNVLRGMAFVLVYDEIKCYV 297  
 DB 241 QSGRGADIMYTGVDWCWKRIAKDEGAKAFPGKAMSNVLRGMAFVLVYDEIKCYV 298

RESULT 13

AAU0380  
 ID AAU0380 standard; Protein; 298 AA.

XX AAU0380;

XX 14-FEB-2002 (first entry)

XX Human adenine nucleotide translocator 3 (ANT3).

XX Human, adenine nucleotide translocator; ANT3;

XX mitochondrial matrix protein.

XX Homo sapiens.

XX WO200185944-A2.  
 XX 15-NOV-2001.  
 XX 11-MAY-2001; 2001WO-US5416.  
 XX 11-MAY-2000; 2000US-0556327.  
 XX (MITO-) MITOKOR.  
 XX Anderson CM, Davis RB, Clevenger W, Wiley SE, Miller SW, Szabo TR,  
 XX Ghosh SS, Moos WH, Pei Y, Carroll AK,  
 XX WPI: 2002-055598/07.  
 XX N-PSDB; AAS16690.  
 XX Novel recombinant expression construct for producing adenine nucleotide  
 XX translocator polypeptides, comprises a regulated promoter linked to  
 XX nucleic acid encoding the polypeptide -  
 XX  
 XX Example 3; Fig 2; 147pp; English.  
 XX The invention relates to a recombinant expression construct (I)  
 XX comprising a regulated promoter operably linked to a nucleic acid  
 XX encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 XX proteins mediate the exchange of ATP synthesised in the mitochondrial  
 XX matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 XX ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 XX culturing the host cell. (I) is also useful for targeting a polypeptide  
 XX of interest to a mitochondrial membrane, where ANT polypeptide is  
 XX expressed as a fusion protein with the polypeptide of interest.  
 XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 XX useful for identifying an agent that binds to an ANT polypeptide. ANT  
 XX ligand is useful for determining the presence of an ANT polypeptide,  
 XX preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 XX ANT from a biological sample, where the ANT ligand is covalently or non-  
 XX covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 XX useful for identifying an agent that interacts with an ANT polypeptide.  
 XX The present sequence represents the amino acid sequence of human ANT3.  
 XX  
 XX Sequence 298 AA;  
 XX  
 XX Query Match 89.2%; Score 1385.5; DB 23; Length 298;  
 XX Best Local Similarity 87.2%; Pred. No. 1.5e-153;  
 XX Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGDHWSFLKDFLAGAANAASKTAVAPIERVKLLQVQASKOISAEKQYKGIIDCVR 60  
 DB 1 MTEQALISFADKPLAGGIAAISKTRAVAPIERVKLLQVQASKOIADKQKGIIDCVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVRHKOFRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVRHKOFRYFAGNLASG 120  
 QY 121 GAAATSTLCFYVPLDPAFTRLAADVGR-AQREPHGIDGCIKIFKSGKAGLYQGRNVS 179  
 DB 121 GAAATSTLCFYVPLDPAFTRLAADVGRSGTERBPGADCIWKTKSGINGLYQGRSVS 180  
 QY 180 VQGIITVRAAFYGVYDZAKGMLPDKNVHI FVSNMIAQSVTAVALGLSTPDTYRRMM 239  
 DB 181 VQGIITVRAAFYGVYDZAKGMLPDKNVHI FVSNMIAQSVTAVALGLSTPDTYRRMM 240  
 QY 240 QSGRKGADIMYTGVDGCRKIAKDEGAKAFKGAWSNVLKMGCAFVLVLDLKKVY 297  
 DB 241 QSGRKGADIMYTGVDGCRKIRFDEGKAFKGAWSNVLKMGCAFVLVLDLKKVY 298

XX 22-OCT-2001 (first entry)  
 XX Human polypeptide SEQ ID NO 6358.  
 XX Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;  
 XX peripheral nervous system; neuropathy; central nervous system; CNS;  
 XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 XX chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 XX leukaemia.  
 XX Homo sapiens.  
 XX WO200153312-A1.  
 XX 26-JUL-2001.  
 XX 26-DEC-2000; 2000WO-US34263.  
 XX 21-JAN-2000; 2000US-0488725.  
 XX 25-APR-2000; 2000US-0552317.  
 XX 09-JUL-2000; 2000US-0598042.  
 XX 19-JUL-2000; 2000US-0620312.  
 XX 03-AUG-2000; 2000US-0653450.  
 XX 14-SEP-2000; 2000US-0662191.  
 XX 19-OCT-2000; 2000US-0683036.  
 XX 29-NOV-2000; 2000US-0727344.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 XX Wang J, Wang Z, Wehrman T, Xu C, Xue AD, Yang Y, Zhang J;  
 XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX WPI: 2001-442253/47.  
 XX N-PSDB; AAI60583.  
 XX Novel nucleic acids and polypeptides, useful for treating disorders  
 XX such as central nervous system injuries -  
 XX  
 XX Example 2; SEQ ID NO 6358; 10078pp; English.  
 XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 XX the encoded polypeptides (AA438642-AA442213) with nootropic,  
 XX immunosuppressant and cytostatic activity. The polynucleotides are useful  
 XX in gene therapy. A composition containing a polypeptide or polynucleotide  
 XX of the invention may be used to treat diseases of the peripheral nervous  
 XX system, such as peripheral nervous injuries, peripheral neuropathy and  
 XX localised neuropathies and central nervous system diseases, such as  
 XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 XX utilisation of the activities such as: Immune system suppression,  
 XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 XX assays for receptor activity, arthritis and inflammation, leukemias and  
 XX C.N.S disorders.  
 XX Note: The sequence data for this patent did not form part of the printed  
 XX specification.  
 XX Sequence 323 AA;  
 XX  
 XX Query Match 89.2%; Score 1385.5; DB 22; Length 323;  
 XX Best Local Similarity 87.2%; Pred. No. 1.7e-153;  
 XX Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGDHWSFLKDFLAGAANAASKTAVAPIERVKLLQVQASKOISAEKQYKGIIDCVR 60  
 DB 26 MTEQALISFADKPLAGGIAAISKTRAVAPIERVKLLQVQASKOIADKQKGIIDCVR 85  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVRHKOFRYFAGNLASG 120  
 DB 86 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVRHKOFRYFAGNLASG 145

QY 121 GAAGATSLCFYYPIDPARRLAADVGR-AQREPHGLDCCIIFKSPDGLRGLYOGFNVS 179  
 DB 146 GAAGATSLCFYYPIDPARRLAADVGRKSTEREFRGLDCLVKIKYSGIRGLYOGFVS 205  
 QY 180 VGGIITVRAAAYFGVYDTAKGMLPDPKXNHIFVSMWIAQSV-TAVAGLISYPPDT--VRR 236  
 DB 206 VGGIITVRAAAYFGVYDTAKGMLPDPKXNHIFVSMWIAQSV-TAVAGLISYPPDTVRRMM 265  
 QY 240 QSGRGADIMYTGVDCCWRKIAKDEGAKAFPKGAMSNVLRGMGAFVVLVDLKKV 297  
 DB 266 QSGRGADIMYTGVDCCWRKIFRDEGKAFPKGAMSNVLRGMGAFVVLVDLKKV 323

## RESULT 15

ABG15423  
 ID ABG15423 standard; Protein; 325 AA.

AC ABG15423;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #15414.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSB-) HYSBQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS79610.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

PS Claim 20; SEQ ID No 45782; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 325 AA;  
 Query Match 83.4%; Score 1294.5; DB 22; Length 325;  
 Best Local Similarity 83.4%; Pred. No. 8e-143;  
 Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4;  
 QY 1 MGDHAFPLKDFLAGAVALAAVSKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCVR 60  
 DB 24 MTDAAVSPAKDFLAGVAAAIKTAVAPIERVKLLLOVQHASKOIADKQYKGIIGCVR 83  
 QY 61 IPKEQGLSFWRGLANVIRYPTQALNFAKDKYKQIFLGVDNRHQFWRYPAGNLASG 120  
 DB 84 IPKEQGLSFWRGLANVIRYPTQALNFAKDKYKQIFLGVDNRHQFWRYPAGNLASG 143  
 QY 121 GAAGATSLCFYYPIDPARRLAADVGR-AQREPHGLDCCIIFKSPDGLRGLYOGFNVS 179  
 DB 144 GAAGATSLCFYYPIDPARRLAADVGRKSTEREFRGLDCLVKIKYSGIRGLYOGFVS 203  
 QY 180 VGGIITVRAAAYFGVYDTAKGMLPDPKXNHIFVSMWIAQSV-TAVAGLISYPPDT--VRR 236  
 DB 204 VGGIITVRAAAYFGVYDTAKGMLPDPKXNHIFVSMWIAQSV-TAVAGLISYPPDTVRRMM 263  
 QY 237 MMSQGRGADIMYTGVDCCWRKIAKDEGAKAFPKGAMSNVLRGMGAFVVLVDLKKV 295  
 DB 264 EXMQSGRGADIMYTGVDCCWRKIFRDEGKAFPKGAMSNVLRGMGAFVVLVDLKKV 323  
 QY 296 Y 296  
 DB 324 Y 324

Search completed: December 18, 2003, 12:40:46  
 Job time : 37.2542 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:38:52 ; Search time 12.3057 Seconds  
(without alignments)  
1021.178 Million cell updates/sec

Title: US-09-811-131-31

Perfect score: 1553

Sequence: 1 MGDHWSFLDPLAGAVAA.....LRGNGAFVLVDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1553	100.0	297	4	US-09-434-354-47
2	1457.5	93.9	298	3	US-08-961-871-10
3	1391.5	89.6	298	4	US-09-434-354-48
4	1385.5	89.2	298	4	US-09-434-354-49
5	304	19.6	469	4	US-09-96-243-289
6	301	19.4	469	3	US-09-188-930-339
7	301	19.4	469	4	US-09-312-283C-339
8	291	18.7	447	4	US-09-160-119-4
9	291	18.7	674	4	US-09-160-119-2
10	267	17.2	291	4	US-09-501-558-2
11	265.5	17.1	335	4	US-09-482-273-118
12	238	15.3	320	2	US-08-933-750C-12
13	238	15.3	320	2	US-09-234-613-12
14	233.5	15.0	312	3	US-09-142-565-2
15	227	14.6	299	1	US-08-518-878B-56
16	227	14.6	299	2	US-08-470-868A-56
17	227	14.6	309	1	US-08-518-878B-51
18	227	14.6	309	2	US-08-807-861A-51
19	227	14.6	309	2	US-08-470-868A-51
20	227	14.6	309	3	US-09-210-681-51
21	227	14.6	309	3	US-08-946-719A-51
22	227	14.6	309	4	US-09-547-983-51
23	227	14.6	311	2	US-08-775-009-53
24	225	14.5	311	2	US-08-775-009-32
25	222.5	14.3	308	2	US-08-937-466-2
26	222.5	14.3	308	2	US-09-172-528-2
27	222.5	14.3	308	3	US-09-318-199-2

## ALIGNMENTS

28	222.5	14.3	308	3	US-09-503-579-2	Sequence 2, Appl1
29	218.5	14.1	432	2	US-08-937-466-4	Sequence 4, Appl1
30	218.5	14.1	432	2	US-09-172-528-4	Sequence 4, Appl1
31	218.5	14.1	432	3	US-09-318-199-4	Sequence 4, Appl1
32	218.5	14.1	432	3	US-09-503-579-4	Sequence 4, Appl1
33	208.5	13.4	293	4	US-09-501-558-4	Sequence 4, Appl1
34	196.5	12.7	307	2	US-08-807-861A-56	Sequence 56, Appl1
35	196.5	12.7	307	3	US-09-210-681-56	Sequence 56, Appl1
36	196.5	12.7	307	3	US-08-946-719A-56	Sequence 56, Appl1
37	196.5	12.7	307	4	US-09-547-983-56	Sequence 56, Appl1
38	193	12.4	303	1	US-08-294-522B-36	Sequence 36, Appl1
39	192	12.4	303	2	US-08-518-878B-37	Sequence 37, Appl1
40	192	12.4	303	2	US-08-807-861A-37	Sequence 37, Appl1
41	192	12.4	303	2	US-08-470-868A-37	Sequence 37, Appl1
42	192	12.4	303	3	US-09-210-681-37	Sequence 37, Appl1
43	192	12.4	303	3	US-08-946-719A-37	Sequence 37, Appl1
44	192	12.4	303	4	US-09-547-983-37	Sequence 37, Appl1
45	190.5	12.3	306	5	PCT-US94-09799-1	Sequence 1, Appl1

## RESULT 1

US-09-434-354-47  
Sequence 47, Application US/09434354  
Patent No. 6562563  
GENERAL INFORMATION:  
APPLICANT: Murphy, Anne N.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Andreyev, Alexander Y.  
APPLICANT: Frigert, Luciano G.  
APPLICANT: Vellicelebi, Gonul  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
FILE REFERENCE: 660088.433  
CURRENT APPLICATION NUMBER: US/09/434,354  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-434-354-47

Query Match 100.0%; Score 1553; DB 4; Length 297;  
Best Local Similarity 100.0%; Pred. No. 4.2e-172;  
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGDHSFLDPLAGAVAAVSKTAVPIERVLLLOVHASKOISAEKYGIIIDCVR	60
DB	1	MGDHSFLDPLAGAVAAVSKTAVPIERVLLLOVHASKOISAEKYGIIIDCVR	60
QY	61	IPKQGLSTFWRGKLVANVIRYPTQALNFAFKQYKOLFLGVDNRHQFRRYFAGNLASG	120
DB	61	IPKQGLSTFWRGKLVANVIRYPTQALNFAFKQYKOLFLGVDNRHQFRRYFAGNLASG	120
QY	121	GAGATSLCFVYPLDFATRLADVGRRAORBFHGLDCTIIKIFKSGGLRGLYGFVSV	180
DB	121	GAGATSLCFVYPLDFATRLADVGRRAORBFHGLDCTIIKIFKSGGLRGLYGFVSV	180
QY	181	GGIIYAAVFGVYDTAKGLPDKVNHIFVSNMIAQSVTAAGLSYPRDYRRMMQ	240
DB	181	GGIIYAAVFGVYDTAKGLPDKVNHIFVSNMIAQSVTAAGLSYPRDYRRMMQ	240
QY	241	SGRGADIMVTGYDCWRKIAKDEGAKAFPKGAMSNVLRMGAFVLVLYDEIKKYV	297
DB	241	SGRGADIMVTGYDCWRKIAKDEGAKAFPKGAMSNVLRMGAFVLVLYDEIKKYV	297

## RESULT 2

US-08-961-871-10  
Sequence 10, Application US/08961871  
Patent No. 6013858  
GENERAL INFORMATION:  
APPLICANT: Wallace, Douglas C.  
APPLICANT: Graham, Brett H.  
APPLICANT: Macgregor, Grant R.  
TITLE OF INVENTION: Mouse lacking Heart-Muscle Adenine  
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Wmmer and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,871  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/030,017  
FILING DATE: 01-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Feiber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 78-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
FAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-871-10

Query Match 93.6%; Score 1457.5; DB 3; Length 298;  
Best Local Similarity 93.6%; Pred. No. 5.4e-161;  
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRR 60  
DB 1 MGDQALSLFKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRR 60  
QY 61 IPKEQGLSFWRGNLANVIRFPYQALNFAFKDKYKQLFLGVDNRHQMFWRYFAGNLASG 120  
DB 61 IPKEQGLSFWRGNLANVIRFPYQALNFAFKDKYKQLFLGVDNRHQMFWRYFAGNLASG 120  
QY 121 GAAATSLCFYVPLDFARTLADVGR-RAOREPHGLDCTIKIPKSGGLGLXOGFVNS 179  
DB 121 GAAATSLCFYVPLDFARTLADVGR-RAOREPHGLDCTIKIPKSGGLGLXOGFVNS 179  
QY 180 VQGIITRYAAAFYGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVALGLSYPPDVRRRMM 239  
DB 180 VQGIITRYAAAFYGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVALGLSYPPDVRRRMM 239  
QY 240 QSGRKGADIMYTGTLDCWRKIADKDEGAFKFGAMSVNLRGMGAFVLVLYDEIKKY 297  
DB 240 QSGRKGADIMYTGTLDCWRKIADKDEGAFKFGAMSVNLRGMGAFVLVLYDEIKKY 298

RESULT 3  
US-09-434-354-48

Sequence 48, Application US/09434354  
Patent No. 6562563  
GENERAL INFORMATION:  
APPLICANT: Murphy, Anne N.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Bileen  
APPLICANT: Andreyev, Alexander Y.  
APPLICANT: Frigieri, Luciano G.  
APPLICANT: Velicelbi, Gonul  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
FILE REFERENCE: 660088.433  
CURRENT APPLICATION NUMBER: US/09/434,354  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 48  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-434-354-48

Query Match 89.6%; Score 1391.5; DB 4; Length 298;  
Best Local Similarity 89.6%; Pred. No. 2.5e-153;  
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRR 60  
DB 1 MTDALSLPDKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRR 60  
QY 61 IPKEQGLSFWRGNLANVIRFPYQALNFAFKDKYKQLFLGVDNRHQMFWRYFAGNLASG 120  
DB 61 IPKEQGLSFWRGNLANVIRFPYQALNFAFKDKYKQLFLGVDNRHQMFWRYFAGNLASG 120  
QY 121 GAAATSLCFYVPLDFARTLADVGR-RAOREPHGLDCTIKIPKSGGLGLXOGFVNS 179  
DB 121 GAAATSLCFYVPLDFARTLADVGR-RAOREPHGLDCTIKIPKSGGLGLXOGFVNS 179  
QY 180 VQGIITRYAAAFYGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVALGLSYPPDVRRRMM 239  
DB 180 VQGIITRYAAAFYGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVALGLSYPPDVRRRMM 240  
QY 240 QSGRKGADIMYTGTLDCWRKIADKDEGAFKFGAMSVNLRGMGAFVLVLYDEIKKY 296  
DB 241 QSGRKGADIMYTGTLDCWRKIADKDEGAFKFGAMSVNLRGMGAFVLVLYDEIKKY 297

RESULT 4  
US-09-434-354-49  
Sequence 49, Application US/09434354  
Patent No. 6562563  
GENERAL INFORMATION:  
APPLICANT: Murphy, Anne N.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Bileen  
APPLICANT: Andreyev, Alexander Y.  
APPLICANT: Frigieri, Luciano G.  
APPLICANT: Velicelbi, Gonul  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
FILE REFERENCE: 660088.433  
CURRENT APPLICATION NUMBER: US/09/434,354  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 49  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien



US-09-434-354-49

Query Match 89.2%; Score 1385.5; DB 4; Length 298;  
Best Local Similarity 87.2%; Pred. No. 1.3e-152;  
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWSLKDFPLGVAVAASKTVAPIERVKLLIQVHASKQISAEKQYGIIDCVR 60  
DB 1 MTEQALISAKDFPLGVAIAASKTRVAPIERVKLLIQVHASKQISADKQYGIIDCVR 60  
QY 61 IPKQGLSPFRKGLNANVIRYFPQALNFAFKDKKYLFGGVDRHKKQPMRYFAGNLASG 120  
DB 61 IPKQGLSPFRKGLNANVIRYFPQALNFAFKDKKYLFGGVDRHKKQPMRYFAGNLASG 120  
QY 121 GAAATSTLCFYPPDPAFTRLAADVGR-AQREFFGLDDCIITKFKSGMLGLYQGFVNS 179  
DB 121 GAAATSTLCFYPPDPAFTRLAADVGRSGTERBFGGLDDCIITKSGMLGLYQGFVNS 180  
QY 180 VQGIITPAAYFGVYDTAKGMLPDPKXVHIFVSNMIAQSYTAVALSLSPDPTVRRMM 239  
DB 181 VQGIITPAAYFGVYDTAKGMLPDPKXVHIFVSNMIAQSYTAVALSLSPDPTVRRMM 240  
QY 240 QSGRKGADIMVTGTVDCWRKXIAKDEGAKAFKGAWSNVLRGMGAPVLVLYDKIKCV 297  
DB 241 QSGRKGADIMVTGTVDCWRKXIFRDEGKAFKGAWSNVLRGMGAPVLVLYDKIKCV 298

## RESULT 5

US-09-966-243-289

Sequence 289, Application US/09996243

Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Bakstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gutney, Austin L.

APPLICANT: KJavlin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C13

CURRENT APPLICATION NUMBER: US/09/996,243

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
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PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598

PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089601  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 19.6%; Score 304; DB 4; Length 469;  
Best Local Similarity 29.0%; Pred. No. 1.4e-26;  
Matches 88; Conservative 58; Mismatches 115; Indels 42; Gaps 11;

QY 6 WSPFKDPLAGAAVAASKTAVAPIERVYLLQVGHASKQISAEKQYKGIIDCVVRIPEQ 65  
DB WRHL---VAGGGAAGAVRTCTAPLDRKVLMOV-HASR-----SNMNGIVGGFTQMTREG 237  
QY 66 GFISFMRGNLANVIRYPTQALNPAFKDKYKOLFQGVDR-----HKQFMYRFGNTLASG 120  
DB GARSIMRGNINVLKIPESAIKFMAYEQIRLV--GSDQETLRHER-----LVAG 287  
QY 121 GAAGNTSLCFYPPDPARTRLAADVGRRAQREFFGLDCTIKIRKSDGLRGLYGFENVSV 180  
DB 288 SIAGLIAOSTIYEMEVKTRMAL---RKTGQYSGMDCCARILARGVAAFYGYFPNM 343  
QY 181 QGITIYRAAYGVVDYAKGM-----LPPKVVHIFVSWMIASVTAVAGLSTYPPDT 232  
DB 344 LGITFYAGIDLAVETLKNMLOHYAVNSADP---GIFVLACGTMSTGQLASSTPLAL 400  
QY 233 VRRBMNQSGRKADIMYTGTVDCMRKIANDEGAKAPFKGMSVNLGMSGAPV-LVLYD 291  
DB 401 VRTMQAASIEGAPVETMSL--FKHILRTREGAFGLRYGLAPFMKVI PAVSISVYVE 458  
QY 292 EIK 294  
DB 459 NLK 461

RESULT 6  
US-09-188-930-339  
Sequence 339; Application US/09188930A  
Patent No. 6150502.  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Murist, Rene  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
FILE REFERENCE: 11000.1011c1  
CURRENT APPLICATION NUMBER: US/09/188, 930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 339  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Mouse  
US-09-188-930-339

Query Match 19.4%; Score 301; DB 3; Length 469;  
Best Local Similarity 28.9%; Pred. No. 3e-26;  
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

QY 6 WSPFKDPLAGAAVAASKTAVAPIERVYLLQVGHASKQISAEKQYKGIIDCVVRI 61  
DB 187 WRHL---VAGGGAAGAVRTCTAPLDRKVLMOV-HASRNNM-----CIVGGFTQMT 233  
QY 62 PKGQGLSFMRGNLANVIRYPTQALNPAFKDKYKOLFQGVDR-----HKQFMYRFGN 116

Db 234 IREGAKSLMKGNGINVLKIPESAIKPMAYEQMKRLV--GSDQETLRIHER----- 283  
Qy 117 LASGAAGATSLCVRYPIDFARTLADVGRRAQREHFGDLCIKIKFKSGLAGLYOGF 176  
Db 284 LVASGLAIAOSSITYPEMEVILKTRMAL---RTKGQYSGLMDCARRIAKGVAAPFKGY 339  
Qy 177 NVSVQGIITYRAAYFGVYDTAKGM-----LPDPKNVHIFVSMMLAQSYTAAG--LIS 227  
Db 340 IPNMLGIIPYAGIDLAAYETIKNTWLORYAVNSADP---GVFV--LACGTISSTCGOLAS 395  
Qy 228 YPFPTVRRMMQSGRKADIMYTGTVDCMKRIAKDEGAKAFPKGANSVLRKMGGAFFV- 286  
Db 396 YPLALVTRMQAQSIEGAPETWSSL--FKQILRTBGAFLYRGLAPNFKVIPAIVSIS 453  
Qy 287 LVLYDEIK 294  
Db 454 YVYVENLK 461

## RESULT 7

US-09-312-283C-339  
; Sequence 339, Application US/09312283C  
; Patent No. 6573095  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Muriison, James G.  
; APPLICANT: Kumble, Krishanand D.  
; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1011c2  
; CURRENT APPLICATION NUMBER: US/09/312, 283C  
; NUMBER OF SEQ ID NOS: 425  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 339  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-312-283C-339

Query Match 19.4%; Score 301; DB 4; Length 469;  
Best Local Similarity 28.9%; Pred. No. 3e-26;  
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;  
Qy 6 WSPFLDPLAGAAVAASKTAVAPIERVDLLQVOHASKQISAEKQYKGIIDCVV---RI 61  
Db 187 WRHL---VAGGGAAGAVRRTCTAPLDRLKVLMOV--HASSNNM-----CIVGGFTQM 233  
Qy 62 PKEQGLSPWRGNLANIYRFPYTOALNFAFDKTKQFLGVDV---HKQFWRYPAGN 116  
Db 234 IREGAKSLMKGNGINVLKIPESAIKPMAYEQMKRLV--GSDQETLRIHER----- 283  
Qy 117 LASGAAGATSLCVRYPIDFARTLADVGRRAQREHFGDLCIKIKFKSGLAGLYOGF 176  
Db 284 LVASGLAIAOSSITYPEMEVILKTRMAL---RTKGQYSGLMDCARRIAKGVAAPFKGY 339  
Qy 177 NVSVQGIITYRAAYFGVYDTAKGM-----LPDPKNVHIFVSMMLAQSYTAAG--LIS 227  
Db 340 IPNMLGIIPYAGIDLAAYETIKNTWLORYAVNSADP---GVFV--LACGTISSTCGOLAS 395  
Qy 228 YPFPTVRRMMQSGRKADIMYTGTVDCMKRIAKDEGAKAFPKGANSVLRKMGGAFFV- 286  
Db 396 YPLALVTRMQAQSIEGAPETWSSL--FKQILRTBGAFLYRGLAPNFKVIPAIVSIS 453  
Qy 287 LVLYDEIK 294  
Db 454 YVYVENLK 461

## RESULT 8

US-09-160-119-4  
; Sequence 4, Application US/09160119A  
; Patent No. 6316219  
; GENERAL INFORMATION:  
; APPLICANT: KRIEF, STEPHANE  
; APPLICANT: SOUCHET, MICHEL  
; APPLICANT: BRILL, ANTOINE  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30985  
; CURRENT APPLICATION NUMBER: US/09/160, 119A  
; CURRENT FILING DATE: 1998-09-24  
; EARLIER APPLICATION NUMBER: EP 97402511.6  
; EARLIER FILING DATE: 1997-10-23  
; EARLIER APPLICATION NUMBER: EP 98401655.0  
; EARLIER FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-160-119-4

Query Match 18.7%; Score 291; DB 4; Length 447;  
Best Local Similarity 27.5%; Pred. No. 4.1e-25;  
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

Qy 12 PLAGAAVAASKTAVAPIERVDLLQVOHASKQISAEKQYKGIIDCVRIPEKQGLSEFW 71  
Db 104 FGLGSVAGAVGATVYVIDVKTMOQSRSTGSFVGLMYNNSPDCFKVLRYGFFGLY 163  
Qy 72 RGNLANIYRFPYTOALNFAFDKTKQFLGVDVRRHKQPMRYFRAGNLSAGGAATSLCFV 131  
Db 164 RGLLPOLGVAPEKAIKLTVDVFRDKFM---HXGQSVPLAEIILAGGCGAGSQTFT 218  
Qy 132 YPLDFAFTRL--AADV--GRRAGREHFGDLCIKIKFKSGLAGLYOGFNVSVQGIITYR 187  
Db 219 NPLIYVIRLQVAGEITGTRVS-----ALSVRDGFRGITYKGAACAFRLDIPFS 269  
Qy 188 AAYFGVYDTAKGMLPDPKNVHIFVSMMLAQSYTAAG--AGLLSYPTVRRMMQSGRGA 246  
Db 270 AIYPPCYAHVYASFANDQGVSPSILLAGIAGMPAASIVTPADVITKR--LQVAARAG 327  
Qy 247 DIWYTGTVDCMKRIAKDEGAKAFPKGANSVLRKMG--APVLYYDEIKKY 296  
Db 328 QTYTSGVIDFRLKILREBGPALMKGAGAVFRSSPQFGVTLTYELLQRW 378

## RESULT 9

US-09-160-119-2  
; Sequence 2, Application US/09160119A  
; Patent No. 6316219  
; GENERAL INFORMATION:  
; APPLICANT: KRIEF, STEPHANE  
; APPLICANT: SOUCHET, MICHEL  
; APPLICANT: BRILL, ANTOINE  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30985  
; CURRENT APPLICATION NUMBER: US/09/160, 119A  
; CURRENT FILING DATE: 1998-09-24  
; EARLIER APPLICATION NUMBER: EP 97402511.6  
; EARLIER FILING DATE: 1997-10-23  
; EARLIER APPLICATION NUMBER: EP 98401655.0  
; EARLIER FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-160-119-2

Query Match 18.7%; Score 291; DB 4; Length 674;

Best Local Similarity 27.5%; Pred. No. 7.7e-25;  
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

QY 12 FLAGAANAASVETAPAPIERVELLLQVQHASKQISAEQYKGIIDCVRIPEKQGLFPM 71  
DB 331 FGLSVAAGVATVATVYFDLTKTRQNGRSTGSPFGLMTKNSPFCFKVLRVBEFFLY 390  
QY 72 RGNLANVIRYPPQALNFAFDKQKQLFLGGVDRHKQFWRYPAGNLASGAAGATSLCFV 131  
DB 391 RGLLPOLLGVAPEKAIKLTVDNFVADKTM-----HKDSVPLAAEIILAGGAGGSQVIFT 445  
QY 132 YPLDPAFRL--AADV--GRRAQRFHGLGDCIITKIFSDGLRGVYGFENNVSGIITXR 187  
DB 446 NPLEIVKIRLQVAGSITTTGPRVS-----ALSVDLGFPGIYKAKACFLTDIPFS 496  
QY 188 AAFGVYDTAKGMLPDPKGVHIFVSMIAQSVTAV-AGILSYPTVRRMMQSGRKA 246  
DB 497 AIFPCVAVKASPNEDGQVSPGSLLAGALAGMPSLVTPADVITR--LQVAAAG 554  
QY 247 DIMYTGVDCKRKIAKDEGAKAFPKGAMSNVLRGKG-APVLVLYDEIKY 296  
DB 555 QTVSGVIDCERKILREBGPALMKAGARVRSPOFGVTLTYELLQRW 605

RESULT 10  
US-09-501-558-2  
; Sequence 2, Application US/09501558  
; Patent No. 6403784  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Zambrowicz, Brian  
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and  
; FILE REFERENCE: Polynucleotides Encoding the Same  
; CURRENT APPLICATION NUMBER: US/09/501,558  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-501-558-2

Query Match 17.2%; Score 267; DB 4; Length 291;  
Best Local Similarity 28.4%; Pred. No. 1.3e-22;  
Matches 84; Conservative 51; Mismatches 137; Indels 24; Gaps 9;

QY 10 KDFLAGAANAASVETAPAPIERVELLLQVQHASKQIS-AEQYKGIIDCVRIPEKQGL 68  
DB 7 KPFYVGLASITAEGETPFDLTKTRLQIQGTINDAKFKEIRYRGMALVIRIGREGLK 66  
QY 69 SFWGNLANVIRYPPQALNFAFDKQKQLFLGGVDRHKQFWRYPAGNLASGAAGATSL 128  
DB 67 AYSGLASIPAMLRQASVGTIKIGTYSGLKRLF---TERED--ETLPINVTGIGISGVSS 121  
QY 129 CFVVPDPAFRLTADVGRRAQRFHGLGDCIITKIFSDGLRGVYGFENNVSGIITXR 188  
DB 122 TIANFTDVKTRMQA-----QSNTTQGMIGMFMNIIYQGBTGRLKQVSLTRQRAIYVG 177  
QY 189 AAFGVYDTAK-----GMLPDPKGVHIFVSMIAQSVTAVAG-ILSYPTVRRMMQOS 241  
DB 178 VEPYVYDITKGLILISGMGDTLVYTHPSSF-----TGLGALASNPVDVVRTRMMQR 232  
QY 242 G-RKADIMYTGVDCKRKIAKDEGAKAFPKGAMSNVLR-GMGAPVLVLYDEIKY 295  
DB 233 VLDRGRCGSGYTGTDCLLQVWKNBGFALYKGFWMNMLRIGPMNIIFFVLYEOLKX 288

RESULT 11  
US-09-482-273-118

Sequence 118, Application US/09482273  
; Patent No. 6534631  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/482,273  
; EARLIER FILING DATE: 2000-01-13  
; EARLIER APPLICATION NUMBER: PCT/US99/15849  
; EARLIER FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,922  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/092,956  
; EARLIER FILING DATE: 1998-07-15  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 118  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: SITE  
; LOCATION: (335)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-482-273-118

Query Match 17.1%; Score 265.5; DB 4; Length 335;  
Best Local Similarity 30.0%; Pred. No. 2.4e-22;  
Matches 89; Conservative 43; Mismatches 138; Indels 27; Gaps 10;

QY 10 KDFLAGAANAASVETAPAPIERVELLLQVQHASKQIS--EQYKGIIDCVRIPEKQ 66  
DB 51 KPFYVGLASITAEGETPFDLTKTRLQVQ--GQSIDARFKIRKGMFHALFRICKEEG 108  
QY 67 FLSTWRGNLANVIRYPPQALNFAFDKQKQLFLGGVDRHKQFWRYPAGNLASGAAGAT 126  
DB 109 VLAYSGLAPALNQAQSVGTIKIGTYSGLKRLF---VERLED--ETLINNIGVSGVT 163  
QY 127 SLCFVVPDPAFRLTADVGRRAQRFHGLGDCIITKIFSDGLRGVYGFENNVSGIITXR 186  
DB 164 SSTIANFTDVKTRMQA--GSLPQSGMTG---STIDIQGBTGRLKQVSLTRQRAIY 219  
QY 187 RAAYGVYDTAK-----GMLPDPKGVHIFVSMIAQSVTAVAG-ILSYPTVRRMM 239  
DB 220 VGVLPYVDITKGLILISGMGDTLTH-----FVSFTGIALGALASNPVDVVRTRMM 274  
QY 240 QSGRKADIMYTGVDCKRKIAKDEGAKAFPKGAMSNVLR-GMGAPVLVLYDEIKY 295  
DB 275 QRAIVGHVDLVKGYTVDGILKWKHKBGFALYKGFWMNMLRIGPMNIIFFVLYEOLK 331

RESULT 12  
US-08-933-750C-12  
; Sequence 12, Application US/08933750C  
; Patent No. 5932442  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti.  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shan, Putvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA

COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,750C  
FILING DATE: September 23, 1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0356 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 320 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: SPLNNO702  
CLONE: 207452  
US-08-933-750C-12

Query Match 15.3%; Score 238; DB 2; Length 320;  
Best Local Similarity 23.5%; Pred. No. 3.6e-19;  
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;

QY 13 LAGVAAVSKTAVPIERVYLLQVQHAS-KQISAQKQYKGIIDCVRIIPKQGFSLFW 71  
DB 20 VAGSVGLVTRALISPPDVAKIRPOLQHERLSRSDPAKXHGIIQASRQIIQEBGPFAFW 79  
QY 72 RGNLANVIRYPTQALNF-AFKDKYKQFLGVDVRHKKQFWRYPAGNLAGGAAGATSLCF 130  
DB 80 KGHVPAQILSIGVAVGFLSFEMLTELVRHGSVYDAEFVHF-VCGGLAACMAITLT 135  
QY 131 VYPLDPARTLADVGRARQREPHGLDCLIKIFKSGDLRGLYQGFVNSVQGIITRYAAY 190  
DB 136 VHPVDVLRTRPALA---QGBPKVYNTLNRHVGWTVRSRGPQVFFKGLAPTLIALIFPYAGLQ 192  
QY 191 FGVDYTRAKGMLPDPKQVHIFVSNMI-----AQSVTAVAGLSTYFPDVR 235  
DB 193 FSCYSSILK-----HLV-KMAIPAEKKNENIQLLCSGAGVISTKITLTPDLDFPK 242  
QY 236 RMMN---QSGRK--GADIMYGTVDQWRKIAKDEGAKAFPGKAMSNYLR-GMGAFVLYL 289  
DB 243 RLVQVGFEHARAARFGQVRYKGLMDCAKQVLOKRGALGFPGKSPSLKALSTGFMEFS 302  
QY 290 YD 291  
DB 303 YE 304

RESULT 13  
US-09-234-613-12  
Sequence 12, Application US/09234613  
Patent No. 6132973  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Bandman, Olga  
APPLICANT: Shah, Purvi  
APPLICANT: Au-Young, Janice  
APPLICANT: Yue, Henry

APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/234,613  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,750  
FILING DATE: September 23, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0356 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 320 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: SPLNNO702  
CLONE: 207452  
US-09-234-613-12

Query Match 15.3%; Score 238; DB 3; Length 320;  
Best Local Similarity 23.5%; Pred. No. 3.6e-19;  
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;

QY 13 LAGVAAVSKTAVPIERVYLLQVQHAS-KQISAQKQYKGIIDCVRIIPKQGFSLFW 71  
DB 20 VAGSVGLVTRALISPPDVAKIRPOLQHERLSRSDPAKXHGIIQASRQIIQEBGPFAFW 79  
QY 72 RGNLANVIRYPTQALNF-AFKDKYKQFLGVDVRHKKQFWRYPAGNLAGGAAGATSLCF 130  
DB 80 KGHVPAQILSIGVAVGFLSFEMLTELVRHGSVYDAEFVHF-VCGGLAACMAITLT 135  
QY 131 VYPLDPARTLADVGRARQREPHGLDCLIKIFKSGDLRGLYQGFVNSVQGIITRYAAY 190  
DB 136 VHPVDVLRTRPALA---QGBPKVYNTLNRHVGWTVRSRGPQVFFKGLAPTLIALIFPYAGLQ 192  
QY 191 FGVDYTRAKGMLPDPKQVHIFVSNMI-----AQSVTAVAGLSTYFPDVR 235  
DB 193 FSCYSSILK-----HLV-KMAIPAEKKNENIQLLCSGAGVISTKITLTPDLDFPK 242  
QY 236 RMMN---QSGRK--GADIMYGTVDQWRKIAKDEGAKAFPGKAMSNYLR-GMGAFVLYL 289  
DB 243 RLVQVGFEHARAARFGQVRYKGLMDCAKQVLOKRGALGFPGKSPSLKALSTGFMEFS 302  
QY 290 YD 291  
DB 303 YE 304

RESULT 14  
US-09-142-565-2

Sequence 2, Application US/09142565A  
 Patent No. 6187560  
 GENERAL INFORMATION:  
 APPLICANT: Lee James Beeley  
 APPLICANT: Kelly Paine  
 APPLICANT: Robert James  
 TITLE OF INVENTION: NOVEL COMPOUNDS  
 FILE REFERENCE: GH-30002  
 CURRENT APPLICATION NUMBER: US/09/142,565A  
 CURRENT FILING DATE: 1999-06-30  
 EARLIER APPLICATION NUMBER: 9704551.2  
 EARLIER FILING DATE: 1997-03-05  
 EARLIER APPLICATION NUMBER: 9705614.7  
 EARLIER FILING DATE: 1997-03-18  
 EARLIER APPLICATION NUMBER: 97305305.1  
 EARLIER FILING DATE: 1997-07-16  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FASTSEQ for Windows Version 3.0  
 SEQ ID NO 2  
 LENGTH: 312  
 TYPE: PRT  
 ORGANISM: HOMO SAPIEN  
 US-09-142-565-2

Query Match 15.0%; Score 233.5; DB 3; Length 312;  
 Best Local Similarity 24.7%; Pred. No. 1.2e-18;  
 Matches 73; Conservative 53; Mismatches 145; Indels 25; Gaps 8;

QY 12 FLAGAANAASKTAVAPIERYKLLQVOHASK--QYKGIIDCVVRIPKEOGL 69  
 DB 17 FLAGACTAACIADLTFFLDTRAKVRLQIGBSQGFVRAVSAQYRGWGTILTWRTGPR 76  
 QY 70 FWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKKQFWRYPAGNLASGAAGATSL 128  
 DB 77 PYNGLVAGLQROMSPASIRIGLYDSVKQYTPKADNSLTLRIIA-----GCTTGAMAV 131  
 QY 129 CFVYPLDPAARLADV---GRRARERHGLGDCIIKIFKSDGLGLYOGFNVSVQGIIT 185  
 DB 132 TCAOPTDVVKRFOQAPRAGGRYOSTVNAKYTTIABEGFRGLMKGTSPVARNALVNC 191  
 QY 186 YRAAYFGVYDTAKGMLPDPKKNVHIFVSMIAQSVTA-----VAGLSYFPTVRRMMQ 240  
 DB 192 VNCBAVVTYDIKEKLD---YHLUTDNPFCHFVSAFAGAFYVAVPVDVVKRYM-- 246  
 QY 241 SGRKADIMYTGVDGWRKIADDEGAKAFPKGAMSNVLR-GMGAFVLYLYDEIKK 295  
 DB 247 ---NSPPQGYSPIDCMIKMVAQEGPTAFYKGFPTSPFLRSGMNVVMFVTEQLKR 299

RESULT 15  
 US-08-518-878B-56  
 Sequence 56, Application US/08518878B  
 Patent No. 5702902  
 GENERAL INFORMATION:  
 APPLICANT: Tartaglia, Louis A.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edwards  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/518,878B  
 FILING DATE: 23-AUG-1995

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cortuzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7853-036  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 INFORMATION FOR SEQ ID NO: 56:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 299 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 US-08-518-878B-56

Query Match 14.6%; Score 227; DB 1; Length 299;  
 Best Local Similarity 23.8%; Pred. No. 6.2e-18;  
 Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

QY 12 FLAGAANAASKTAVAPIERYKLLQVOHASK--QISAEKQYKGIIDCVVRIPKEOGL 68  
 DB 7 FLAGACTAACIADLTFFLDTRAKVRLQIGBSQGFVRAVSAQYRGWGTILTWRTGPR 66  
 QY 69 SFRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKKQFWRYPAGNLASGAAGATSL 128  
 DB 67 SLVNGLVAGLQROMSPASIRIGLYDSVKQFYTKGSEHAS-----IGSRLLAGSTTGALAV 121  
 QY 129 CFVYPLDPAARLADVGRARERHGLGDCIIKIFKSDGLGLYOGFNVSVQGIIT 188  
 DB 122 AVAOPTDVVKRFOQAPRAGGRYOSTVNAKYTTIABEGFRGLMKGTSPVARNALVNC 181  
 QY 189 AYFGVYDTAK-----GMLPDPKKNVHIFVSMIAQSVTAAGLSYFPTVRRMMQSG 242  
 DB 182 AELVYTDLIDKALLKANLMTDLDLPCF--FTSAFAGFCTTV---IASVVDVVKRYM----- 233  
 QY 243 RKGADIMYTGVDGWRKIADDEGAKAFPKGAMSNVLR-GMGAFVLYLYDEIKK 295  
 DB 234 -NSALQGYSSAGHCALTMLQKEGPRAFYKGFMPFRLGSMNVVMFVTEQLKR 286

Search completed: December 18, 2003, 12:44:54  
 Job time: 13.3057 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:43:17 ; Search time 24.2768 Seconds  
(without alignments)  
2284.595 Million cell updates/sec

Title: US-09-811-131-31

Perfect score: 1553  
Sequence: 1 MGHASFLKDFLAGVA...LRGMAFVLYDEIKKY 297

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubppaa/PCR\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubppaa/PCRUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*
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- 9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1553	100.0	297	9 US-09-811-094-31	Sequence 31, Appl
2	1553	100.0	297	9 US-09-810-644-31	Sequence 31, Appl
3	1553	100.0	297	10 US-09-185-904A-31	Sequence 31, Appl
4	1391.5	89.6	298	9 US-09-811-094-32	Sequence 32, Appl
5	1391.5	89.6	298	9 US-09-810-644-32	Sequence 32, Appl
6	1391.5	89.6	298	10 US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.2	298	9 US-09-811-094-33	Sequence 33, Appl
8	1385.5	89.2	298	9 US-09-810-644-33	Sequence 33, Appl
9	1385.5	89.2	298	10 US-09-185-904A-33	Sequence 33, Appl
10	773.5	49.6	179	12 US-10-029-386-32501	Sequence 32501, A
11	771	49.6	301	12 US-10-032-585-7194	Sequence 7194, Ap
12	740	47.6	381	12 US-10-141-478A-2	Sequence 2, Appl
13	734	47.3	318	10 US-09-801-368-252	Sequence 252, Appl
14	734	47.3	386	9 US-09-734-569-170	Sequence 170, App
15	703.5	45.3	308	15 US-10-128-714-3338	Sequence 3338, Ap

16	703.5	45.3	308	15	US-10-128-714-8338	Sequence 8338, Ap
17	666	42.9	677	12	US-10-259-165-192	Sequence 192, App
18	461	29.7	132	9	US-09-825-301-1459	Sequence 1459, App
19	402.5	25.9	87	9	US-09-864-761-36440	Sequence 36440, A
20	350.5	22.6	475	10	US-09-777-921A-4	Sequence 4, Appl
21	346.5	22.3	477	10	US-09-777-921A-2	Sequence 2, Appl
22	320.5	20.6	384	12	US-10-094-749-1789	Sequence 1789, Ap
23	312	20.1	410	10	US-09-777-921A-5	Sequence 5, Appl
24	306	19.7	680	12	US-10-291-172-339	Sequence 339, App
25	304	19.6	469	9	US-09-989-722-289	Sequence 289, App
26	304	19.6	469	9	US-09-989-723-289	Sequence 289, App
27	304	19.6	469	9	US-09-989-729-289	Sequence 289, App
28	304	19.6	469	9	US-09-989-727-289	Sequence 289, App
29	304	19.6	469	10	US-09-989-731-289	Sequence 289, App
30	304	19.6	469	10	US-09-989-732-289	Sequence 289, App
31	304	19.6	469	10	US-09-991-073-289	Sequence 289, App
32	304	19.6	469	10	US-09-990-442-289	Sequence 289, App
33	304	19.6	469	10	US-09-991-163-289	Sequence 289, App
34	304	19.6	469	10	US-09-993-604-289	Sequence 289, App
35	304	19.6	469	10	US-09-990-456-289	Sequence 289, App
36	304	19.6	469	10	US-09-989-721-289	Sequence 289, App
37	304	19.6	469	10	US-09-992-596-289	Sequence 289, App
38	304	19.6	469	10	US-09-989-735-289	Sequence 289, App
39	304	19.6	469	10	US-09-989-735-289	Sequence 289, App
40	304	19.6	469	10	US-09-990-444-289	Sequence 289, App
41	304	19.6	469	10	US-09-991-181-289	Sequence 289, App
42	304	19.6	469	10	US-09-989-730-289	Sequence 289, App
43	304	19.6	469	10	US-09-990-436-289	Sequence 289, App
44	304	19.6	469	10	US-09-993-687-289	Sequence 289, App
45	304	19.6	469	11	US-09-989-734-289	Sequence 289, App

## ALIGNMENTS

RESULT 1  
US-09-811-094-31  
Sequence 31, Application US/09811094  
Patent No. US2001004144A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pei, Yashong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D4  
CURRENT APPLICATION NUMBER: US/09/811, 094  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 31  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-811-094-31

Query Match 100.0%; Score 1553; DB 9; Length 297;  
Best Local Similarity 100.0%; Pred. No. 2.3e-160;  
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGHASFLKDFLAGVA...LRTAVAPTEHYLLQVGHASQISAERQKIIIDCVR 60  
DB 1 MGHASFLKDFLAGVA...LRTAVAPTEHYLLQVGHASQISAERQKIIIDCVR 60  
QY 1 IPKGGFLSPWRGNLNVIRYPTQALNFAFKQYKQLFGVGVDRHKQFRRYPAGNIASG 120  
DB 1 IPKGGFLSPWRGNLNVIRYPTQALNFAFKQYKQLFGVGVDRHKQFRRYPAGNIASG 120



QY 121 GAAGATSLCFVYPLDPARTRLAADVGRRAQREHFHGLDCCIIFKSDGLRGLYOGFNVSV 180  
DB 121 GAAGATSLCFVYPLDPARTRLAADVGRRAQREHFHGLDCCIIFKSDGLRGLYOGFNVSV 180  
QY 181 OGIIITRYAAYFGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240  
DB 181 OGIIITRYAAYFGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240  
QY 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297  
DB 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297

## RESULT 2

US-09-810-644-31  
Sequence 31, Application US/09810644  
Patent No. US20020012992A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Miller, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D3  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 31  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-810-644-31

Query Match 100.0%; Score 1553; DB 9; Length 297;  
Best Local Similarity 100.0%; Pred. No. 2.3e-160;  
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
QY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKGFWRYFAGNLASG 120  
DB 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKGFWRYFAGNLASG 120  
QY 121 GAAGATSLCFVYPLDPARTRLAADVGRRAQREHFHGLDCCIIFKSDGLRGLYOGFNVSV 180  
DB 121 GAAGATSLCFVYPLDPARTRLAADVGRRAQREHFHGLDCCIIFKSDGLRGLYOGFNVSV 180  
QY 181 OGIIITRYAAYFGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240  
DB 181 OGIIITRYAAYFGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240  
QY 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297  
DB 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297

## RESULT 3

US-09-185-904A-31  
Sequence 31, Application US/09185904A  
Patent No. US2002017185A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Miller, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
FILE REFERENCE: 660088.420  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 31  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-185-904A-31

Query Match 100.0%; Score 1553; DB 10; Length 297;  
Best Local Similarity 100.0%; Pred. No. 2.3e-160;  
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
QY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKGFWRYFAGNLASG 120  
DB 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKGFWRYFAGNLASG 120  
QY 121 GAAGATSLCFVYPLDPARTRLAADVGRRAQREHFHGLDCCIIFKSDGLRGLYOGFNVSV 180  
DB 121 GAAGATSLCFVYPLDPARTRLAADVGRRAQREHFHGLDCCIIFKSDGLRGLYOGFNVSV 180  
QY 181 OGIIITRYAAYFGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240  
DB 181 OGIIITRYAAYFGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240  
QY 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297  
DB 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297

## RESULT 4

US-09-811-094-32  
Sequence 32, Application US/09811094  
Patent No. US2001004414A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Miller, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D4  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-811-094-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;  
Best Local Similarity 88.6%; Pred. No. 8.3e-143;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
Db 1 MTDALSLAKDFLAGAANAASKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVR 60

Qy 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKQFLGQVDRHKOFRYFAGNLASG 120  
Db 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKQFLGQVDRHKOFRYFAGNLASG 120

Qy 121 GAAGATSLCFYYPDLPARTRLAADVGR-ADREPHGLDCCIIFKSDGLRGLYQGFNV 179  
Db 121 GAAGATSLCFYYPDLPARTRLAADVGR-ADREPHGLDCCIIFKSDGLRGLYQGFNV 180

Qy 180 VGGIITRAAYFGYDPAKGMPLDPKXVHIFVSMIAQSTYAVAGLSTYPTDTRRRMM 239  
Db 180 VGGIITRAAYFGYDPAKGMPLDPKXVHIFVSMIAQSTYAVAGLSTYPTDTRRRMM 240

Qy 240 QSGRKGADIMYTGVDCKRIADKDEGAKAFKGMNSVLRGMGAFVLVLYDEIKKY 296  
Db 241 QSGRKGADIMYTGVDCKRIADKDEGAKAFKGMNSVLRGMGAFVLVLYDEIKKY 297

RESULT 5  
US-09-810-644-32  
Sequence 32, Application US/09810644  
Patent No. US2002012992A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Cleenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Miller, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pel, Yashong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D3  
CURRENT APPLICATION NUMBER: US/09/810.644  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-810-644-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;  
Best Local Similarity 88.6%; Pred. No. 8.3e-143;  
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

RESULT 6  
US-09-185-904A-32  
Sequence 32, Application US/09185904A  
Patent No. US20020177185A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Cleenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Miller, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pel, Yashong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
TITLE OF INVENTION: THEREFOR  
FILE REFERENCE: 660088.420  
CURRENT APPLICATION NUMBER: US/09/185.904A  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-185-904A-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;  
Best Local Similarity 88.6%; Pred. No. 8.3e-143;  
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
Db 1 MTDALSLAKDFLAGAANAASKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVR 60

Qy 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKQFLGQVDRHKOFRYFAGNLASG 120  
Db 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKQFLGQVDRHKOFRYFAGNLASG 120

Qy 121 GAAGATSLCFYYPDLPARTRLAADVGR-ADREPHGLDCCIIFKSDGLRGLYQGFNV 179  
Db 121 GAAGATSLCFYYPDLPARTRLAADVGR-ADREPHGLDCCIIFKSDGLRGLYQGFNV 180

Qy 180 VGGIITRAAYFGYDPAKGMPLDPKXVHIFVSMIAQSTYAVAGLSTYPTDTRRRMM 239  
Db 180 VGGIITRAAYFGYDPAKGMPLDPKXVHIFVSMIAQSTYAVAGLSTYPTDTRRRMM 240

Qy 240 QSGRKGADIMYTGVDCKRIADKDEGAKAFKGMNSVLRGMGAFVLVLYDEIKKY 296  
Db 241 QSGRKGADIMYTGVDCKRIADKDEGAKAFKGMNSVLRGMGAFVLVLYDEIKKY 297

RESULT 7  
US-09-811-094-33  
Sequence 33, Application US/09811094  
Patent No. US2001004414A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Cleenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Miller, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pel, Yashong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D4  
CURRENT APPLICATION NUMBER: US/09/811.094  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 33  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-811-094-33

Query Match 89.2%; Score 1385.5; DB 9; Length 298;  
Best Local Similarity 87.2%; Pred. No. 3.7e-142;  
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
DB 1 MTEQALSPAKDFLAGAANAISKTAVAPIERVKLLQVQHASKOIADKQYGIIDCVR 60  
QY 61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRFFAGNLASG 120  
DB 61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRFFAGNLASG 120  
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFNVS 180  
QY 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSPEDTVRRMM 239  
DB 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGVSPEDTVRRMM 240  
QY 240 QSGRKGADIMYTGVDCKRKIAKDEGAKAFKFGAMSVNLKMGCAFVLVYDELKQYV 297  
DB 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFKFGAMSVNLKMGCAFVLVYDELKQYV 298

#### RESULT 8

US-09-810-644-33  
Sequence 33, Application US/09810644  
Patent No. US20020012992A1

GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Willey, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pel, Yashong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D3  
CURRENT APPLICATION NUMBER: US/09/810,644  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 33  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-810-644-33

Query Match 89.2%; Score 1385.5; DB 9; Length 298;  
Best Local Similarity 87.2%; Pred. No. 3.7e-142;  
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
DB 1 MTEQALSPAKDFLAGAANAISKTAVAPIERVKLLQVQHASKOIADKQYGIIDCVR 60  
QY 61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRFFAGNLASG 120  
DB 61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRFFAGNLASG 120  
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFNVS 179

DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFNVS 180  
QY 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSPEDTVRRMM 239  
DB 181 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGVSPEDTVRRMM 240  
QY 240 QSGRKGADIMYTGVDCKRKIAKDEGAKAFKFGAMSVNLKMGCAFVLVYDELKQYV 297  
DB 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFKFGAMSVNLKMGCAFVLVYDELKQYV 298

#### RESULT 9

US-09-185-904A-33  
Sequence 33, Application US/09185904A  
Patent No. US20020177185A1

GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Willey, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
TITLE OF INVENTION: THEREFOR  
FILE REFERENCE: 660088.420  
CURRENT APPLICATION NUMBER: US/09/185,904A  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 33  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-185-904A-33

Query Match 89.2%; Score 1385.5; DB 10; Length 298;  
Best Local Similarity 87.2%; Pred. No. 3.7e-142;  
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
DB 1 MTEQALSPAKDFLAGAANAISKTAVAPIERVKLLQVQHASKOIADKQYGIIDCVR 60  
QY 61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRFFAGNLASG 120  
DB 61 IPKEGGLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRFFAGNLASG 120  
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFNVS 180  
QY 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSPEDTVRRMM 239  
DB 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGVSPEDTVRRMM 240  
QY 240 QSGRKGADIMYTGVDCKRKIAKDEGAKAFKFGAMSVNLKMGCAFVLVYDELKQYV 297  
DB 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFKFGAMSVNLKMGCAFVLVYDELKQYV 298

#### RESULT 10

US-10-029-386-32501  
Sequence 32501, Application US/10029386  
Publication No. US20030194704A1

GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzen, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: ABOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 32501  
LENGTH: 179  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC004000.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96  
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU2 2.00e-83  
US-10-029-386-32501

Query Match 49.8%; Score 773.5; DB 12; Length 179;  
Best Local Similarity 88.3%; Pred. No. 6.7e-76;  
Matches 144; Conservative 12; Mismatches 6; Indels 1; Gaps 1;

QY 38 VQHASQKQISAKQYKGIIDCVRIPEKQGFSPMGNLANYRYPTQALNFAFKDKYKQ 97  
DB 1 VQHASQKQITADKQYKGIIDCVRIPEKQGFSPMGNLANYRYPTQALNFAFKDKYKQ 60  
QY 98 LFLGVDRHKQFWRYFAAGNLASGGAAGTSLCFVYPLDPAFTRLAADVGR--AQREPHGL 156  
DB 61 IFLGVDRHKQFWRYFAAGNLASGGAAGTSLCFVYPLDPAFTRLAADVGR--AQREPHGL 120  
QY 157 GDCIILKIFKSDGLGGLYGFNVSVQGIITRYRAAYGVYDTAKG 199  
DB 121 GDCIILKIFKSDGLGGLYGFNVSVQGIITRYRAAYGVYDTAKG 163

RESULT 11  
US-10-032-585-7194  
Sequence 7194, Application US/10032585  
Publication No. US20030180953A1  
GENERAL INFORMATION:  
APPLICANT: Terry, Roemer D.  
APPLICANT: Bo, Jlang  
APPLICANT: Charles, Boone  
APPLICANT: Howard, Bussey  
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery  
FILE REFERENCE: 10182-005-999  
CURRENT APPLICATION NUMBER: US/10/032,585  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 8000  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7194  
LENGTH: 301  
TYPE: PRT  
ORGANISM: Candida albicans  
US-10-032-585-7194

Query Match 49.6%; Score 771; DB 12; Length 301;  
Best Local Similarity 53.9%; Pred. No. 2.5e-75;  
Matches 158; Conservative 43; Mismatches 82; Indels 10; Gaps 5;

QY 7 SFLKDFLAGAVALAASVSTAVAPIERVKLLQVQ--HASKQISAKQYKGIIDCVRIPEKQ 65  
DB 5 NFPYDPMAGVSAVSKTAAPIERVKLLQVQ--HASKQISAKQYKGIIDCVRIPEKQ 64  
QY 66 GFLSPMGNLANYRYPTQALNFAFKDKYKQFLGVDRHKQFWRYFAAGNLASGGAAGA 125  
DB 65 GVSFPMGNLANYRYPTQALNFAFKDKYKQFLGVDRHKQFWRYFAAGNLASGGAAGA 122  
QY 126 TSLGCVYPLDPAFTRLAADVGR--AQREPHGLGDCIILKIFKSDGLGGLYGFNVSVQ 182  
DB 123 TSLGCVYPLDPAFTRLAADVGR--AQREPHGLGDCIILKIFKSDGLGGLYGFNVSVQ 182  
QY 183 IITRYRAAYGVYDTAKG--MLDPPKQVHIFVSMMLAQSVTAVALGLSYDPFTRBRMMQ 241

DB 183 IIVYRGALYFGLYDLSLKPVLVLGPLEGSFLASFLGGMVTTTASVASYPLDTRBRMMQ 242  
QY 242 GRKADIMTYGTVDCKRIADDEGAKAFPKGAMSNVIRKMGAGAVLYLYDIK 294  
DB 243 GQA---VYTDGALDCCFRKVAABGVSLFKGCGANILRGVAGAVLSLYDQLQ 292

RESULT 12  
US-10-141-478A-2  
Sequence 2, Application US/10141478A  
Publication No. US20030148300A1  
GENERAL INFORMATION:  
APPLICANT: Valentine, Henry  
APPLICANT: Savage, Thomas  
APPLICANT: Voelker, Toni  
TITLE OF INVENTION: Metabolite Transporters  
FILE REFERENCE: 16515.146  
CURRENT APPLICATION NUMBER: US/10/141,478A  
CURRENT FILING DATE: 2002-05-09  
PRIOR APPLICATION NUMBER: US 60/289,519  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: 60/289,527  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 16517.  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 381  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-141-478A-2

Query Match 47.6%; Score 740; DB 12; Length 381;  
Best Local Similarity 53.6%; Pred. No. 8.1e-72;  
Matches 165; Conservative 39; Mismatches 76; Indels 28; Gaps 8;

QY 7 SFLKDFLAGAVALAASVSTAVAPIERVKLLQVQHASQKQISAK--EKQYKGIIDCVRIPEK 63  
DB 79 NFDLDFLMGVSAAVSTAAPIERVKLLQVQ--DEMIRKGRUSEPYKIGDCFGRTIK 136  
QY 64 EOGFLSPMGNLANYRYPTQALNFAFKDKYKQFLGVDRHKQFWRYFAAGNLASGGA 123  
DB 137 DEFGSLMRGNLANYRYPTQALNFAFKDKYKQFLGVDRHKQFWRYFAAGNLASGGA 195  
QY 124 GATSLCFVYPLDPAFTRLAADVGRBAO---RPFHGLGDCIILKIFKSDGLGGLYGFNV 179  
DB 196 GATSLCFVYPLDPAFTRLAADVGRBAO---RPFHGLGDCIILKIFKSDGLGGLYGFNV 255  
QY 180 VQGIITRYRAAYGVYDTAKG---GMLDPPKQVHIFVSMMLAQSVTAVALGLSYDPFTR 234  
DB 256 CVGIIVYRGALYFGLYDLSLKPVLVLGPLEGSFLASFLGGMVTTTASVASYPLDTRBRMMQ 311  
QY 235 RRMAMQGRKADIMTYGTVDCKRIADDEGAKAFPKGAMSNVIRKMGAGAVLYLYDIK 293  
DB 312 RRMAMQGRKADIMTYGTVDCKRIADDEGAKAFPKGAMSNVIRKMGAGAVLYLYDIK 293  
QY 294 -----KKY 296  
DB 369 LTVRGKTY 376

RESULT 13  
US-09-801-368-252  
Sequence 252, Application US/09801368  
Patent No. US20020128250A1  
GENERAL INFORMATION:  
APPLICANT: Busby, Robert  
APPLICANT: Cali, Brian  
APPLICANT: Hecht, Peter  
APPLICANT: Holtzman, Doug

```

; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silve, Jeff
; APPLICANT: Sumner, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 252
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-801-368-252

Query Match          47.3%; Score 734; DB 10; Length 318;
Best Local Similarity 53.2%; Pred. No. 2.8e-71;
Matches 156; Conservative 45; Mismatches 82; Indels 10; Gaps 5;

OY 7 SFLDPLAGAAVAAVSKTAVPIERVKLLQVQ-HASQISAEKQYKGIIDCVIRIPKQ 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 22 NFLIDPLMGVSAVAAKTAAASPIERVKLLIQDDEMLKQIDLRKTAAGLIDCFKKTATQ 81
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 66 GFLSFRGNLANVIRYPTQALNFAFKQYKQFLFGVDRHQRFPYFAGNLASGAAGA 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 82 GVISWRKGTANVIRYPTQALNFAFKQIKAMF--GRKKGAVAKWFRAGNLASGAAGA 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 126 TSLCFVYPLDPARTRLAAD--VGRARQEPHGLDCLIKIPKSDGLRGLYOGFNVSVQ 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 LSLFVYSLDYARTRLAADSKSSKSGAGAFNGLLIDVVKTKLSDGAVGLYGFPSVVG 199
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 183 IIVYAAAFRGVYDTAKGMLPDPKXVHITV-SWMIAQSVTAVAGLSYPPDTRRRMMQ 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 IVVYGLYFGMDSLKPLLTGSLGSLFASFLGMVVTGTSTGCTSYPLDTRRRMMQ 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 242 GRKGAIDIMYTGVCWRKTIADKGAFAFKGAMSVNLKMGAFVLYLDEIK 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 260 GQA---VKYDGAFLDLKRTKIYVAEGVGLFKGCGANILKGVAGAGVISMVDQ 309
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-09-734-569-170
; Sequence 170, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:
; APPLICANT: Lersch, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reinold, Andreas
; APPLICANT: Cirus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Reeki, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; FILE REFERENCE: BASF-NAE-1332-99-US
; CURRENT APPLICATION NUMBER: US/09/734,569
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; PRIOR FILING DATE: 1999-12-16
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```

; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: Patent in Ver. 2.1/WordPerfect 6.1
; SEQ ID NO: 170
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Physcomitrella patens
; US-09-734-569-170

Query Match          47.3%; Score 734; DB 9; Length 386;
Best Local Similarity 52.9%; Pred. No. 3.7e-71;
Matches 156; Conservative 43; Mismatches 84; Indels 12; Gaps 6;

OY 7 SFLDPLAGAAVAAVSKTAVPIERVKLLQVQ-HASQISAEKQYKGIIDCVIRIPKQ 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 SPMDFLMGVSAVAVSKTAAPIERVKLLIQDDEMLKQIDLRKTAAGLIDCFKKTATQ 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 66 GFLSFRGNLANVIRYPTQALNFAFKQYKQFLFGVDRHQRFPYFAGNLASGAAGA 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 GMSLWRKGTANVIRYPTQALNFAFKDYFSLF--GYKXKDGWTKWFRAGNLASGAAG 201
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 125 ATSLCFVYPLDPARTRLAADYGR--AQRFPHGLDCLIKIPKSDGLRGLYOGFNVSV 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 ASLFLFVYSLDYARTRLAADSKSSKSGAGAFNGLLIDVVKTKLATDGIAGLYGFAISC 261
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 181 OGIIIVYAAAFRGVYDTAKG-MLPDPKXVHITV-SWMIAQSVTAVAGLSYPPDTRRRMM 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 262 AGIIVYRLYGLYDLSLPPVLYGNLBNFLASFLGNGITIGAGLASYPIDTRRRMM 321
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 240 QSRKGAIDIMYTGVCWRKTIADKGAFAFKGAMSVNLKMGAFVLYLDEIK 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 322 TSGRA---VKYNGSMDAPKQILAKGAKSLFKGCGANILKRVAGAGVLSGVDQ 373
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-10-128-714-3338
; Sequence 3338, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengdi
; APPLICANT: Tienhoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Broshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 3338
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-3338

Query Match          45.3%; Score 703.5; DB 15; Length 308;
Best Local Similarity 50.8%; Pred. No. 5.7e-68;
Matches 150; Conservative 45; Mismatches 87; Indels 13; Gaps 6;

OY 7 SFLDPLAGAAVAAVSKTAVPIERVKLLQVQHASQISA--EKQYKGIIDCVIRIPK 63
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```

```

Db      7 APTDFAVGVSAVSKTAAPIERIKL--VONODEMIRAGRLDRKNGIIDCFRTAQ 64
Qy      64 BQPLSFMRGNLANYIRYPTQALNFAFKDKYKQPLGVDNRHQFMRYPAGNLASGGA 123
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65 AEGVMSLMRGNANVIRYPTQALNFAFRDYYKSMFAKKDR-DGYAKMMGNLASGGA 123
Qy      124 GATSLCFYYPPLDPARTRLADVGRR---AOREFHGLADCIIFKSDGLRGLYOGFNVS 180
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      124 GATSLLFYSLDYARTRLANDAKSAGGERQFNGLIDVYRKTILASDGIAGLYRGFSPV 183
Qy      181 OGIIITYRAAYTGVDTAKG-MLPDPKNVHIFVSMNIAQSVTAVAGLSYPFDVRRMM 239
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      184 LGIVVYRGLYFGMYDSIKPVVYVCSLEGSFLASFLIGWTVTGAGIASYPLDTIRRRMM 243
Qy      240 OSGRRGADIMYTGVCWRKTLAKDGAFAFKGAMSNVLRGCGAFVLYDEIK 294
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      244 TSGEA--VKYKSSIDAARQIIRAKGVKSLFKGAGANILRGVAGVLSITYDQV 295

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Search completed: December 18, 2003, 12:55:43  
 Job time : 25.278 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:46 ; Search time 14.3012 Seconds  
(without alignments)  
1997.178 Million cell updates/sec

Title: US-09-811-131-31

Perfect score: 1553

Sequence: 1 MGDHMSFLMDFLAAGAVAA.....LRGNGAFVLVYDEIKKYV 297

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1 A44778	ADP,ATP carrier pr
2	1466.5	94.4	298	2 160173	adenine nucleotide
3	1463.5	94.2	298	1 S37210	ADP,ATP carrier pr
4	1458.5	93.9	298	1 XWBO	ADP,ATP carrier pr
5	1391.5	89.6	298	1 A29132	ADP,ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP,ATP carrier pr
7	1380.5	88.9	298	2 B33646	ADP,ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP,ATP carrier pr
9	1142.5	73.6	301	1 S31935	ADP,ATP carrier pr
10	1045.5	67.3	313	2 T25850	ADP,ATP carrier pr
11	1043.5	67.2	313	2 T23207	ADP,ATP carrier pr
12	1037.5	66.8	300	2 T25371	ADP,ATP carrier pr
13	1005.5	64.7	300	2 T15206	ADP,ATP carrier pr
14	973.5	62.7	339	2 A41677	ADP,ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP,ATP carrier pr
16	772	49.7	306	1 T20012	ADP,ATP carrier pr
17	770.5	49.6	308	1 S30259	ADP,ATP carrier pr
18	756.5	48.7	322	2 T40526	ADP,ATP carrier pr
19	752.5	48.5	322	2 T40526	ADP,ATP carrier pr
20	752.5	48.5	322	2 T40526	ADP,ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP,ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP,ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP,ATP carrier pr
24	745.5	48.0	326	2 T25728	ADP,ATP carrier pr
25	745.5	48.0	386	2 S17917	ADP,ATP carrier pr
26	744.5	47.9	386	2 S19194	ADP,ATP carrier pr
27	740	47.6	379	2 S21313	ADP,ATP carrier pr
28	740	47.6	386	2 S14874	ADP,ATP carrier pr
29	737	47.5	385	1 S29852	ADP,ATP carrier pr

30	736	47.4	307	2 A36582	ADP,ATP carrier pr
31	734	47.3	318	1 A31978	ADP,ATP carrier pr
32	733.5	47.2	313	1 XWNC	ADP,ATP carrier pr
33	729	46.9	303	2 S68154	ADP,ATP carrier pr
34	728.5	46.9	306	2 T42011	ADP,ATP carrier pr
35	718.5	46.3	309	2 A24849	ADP,ATP carrier pr
36	676	43.5	298	2 T24029	ADP,ATP carrier pr
37	508	32.7	327	2 T51577	ADP,ATP carrier pr
38	368	23.7	415	2 T48171	ADP,ATP carrier pr
39	367.5	23.7	325	2 T04273	ADP,ATP carrier pr
40	363	23.4	381	2 T51158	ADP,ATP carrier pr
41	350.5	22.6	475	2 T50686	ADP,ATP carrier pr
42	349.5	22.5	352	2 T01729	ADP,ATP carrier pr
43	345.5	22.2	358	2 T45934	ADP,ATP carrier pr
44	334.5	21.5	348	2 D84798	ADP,ATP carrier pr
45	327	21.1	332	2 T47703	ADP,ATP carrier pr

#### ALIGNMENTS

RESULT 1  
A44778  
ADP,ATP carrier protein T1 - human  
N:Alternate names: mitochondrial ADP,ATP translocase 1  
C:Species: Homo sapiens (man)  
C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
C:Accession: A44778, S03893, A39891, A28116  
R:Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.  
J. Biol. Chem. 264, 13998-14004, 1989  
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located  
A:Reference number: A44778, MUID:89340493, PMID:2547778  
A:Accession: A44778  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <L1A>  
A:Cross-references: GB:004982; NID:g178658; PIND:AAA51736.1; PID:g178659  
R:Cooren, A.L.; Runswick, M.J.; Walker, J.E.  
J. Mol. Biol. 206, 261-280, 1989  
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr.  
A:Reference number: S03893; MUID:89236396; PMID:2541251  
A:Accession: S03893  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-298 <CO2>  
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987  
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader  
A:Reference number: A39891, MUID:86041149; PMID:2823266  
A:Accession: A39891  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>  
A:Cross-references: GB:002966; NID:g339919; PIND:AAA61223.1; PID:g339920  
R:Experimental source: clone pEMANT  
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
A:Reference number: A94197, MUID:86124845; PMID:2829183  
A:Accession: A28116  
A:Molecule type: mRNA  
A:Residues: 1-37 <HOU>  
A:Cross-references: GB:003993; NID:g339724; PIND:AAA6751.1; PID:g339725  
A:Experimental source: liver  
C:Genetics:  
A:Gene: GDB:ANT1, T1  
A:Cross-references: GDB:119680; OMIM:103220  
A:Map position: 4q35-4q35  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C:Keywords: duplication, homodimer; mitochondrial; transmembrane protein  
F:2-298/Protein: ADP,ATP carrier protein #status predicted <MAT>  
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>  
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1; Length 298;  
Best Local Similarity 98.3%; Pred. No. 1.5e-130;  
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
Db 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
Qy 1 IPKQGFSLFMRGNLANVIRFPQALNFAFKDKYKQFLGSDVRHQQPMRYFPGNLASG 120  
Db 1 IPKQGFSLFMRGNLANVIRFPQALNFAFKDKYKQFLGSDVRHQQPMRYFPGNLASG 120  
Qy 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 179  
Db 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 180  
Qy 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMIAQSVTAVALGVSYPDTRRRMM 239  
Db 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMIAQSVTAVALGVSYPDTRRRMM 240  
Qy 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 297  
Db 241 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 298

# RESULT 2

adenine nucleotide translocator - rat

C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
C;Accession: 160173

R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.  
Biochim. Biophys. Acta 1152, 192-196, 1993  
A;Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat  
A;Reference number: 160173; MUID:94002161; PMID:8399300  
A;Accession: 160173

A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-298 <RES>  
A;Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA3842.1; PID:g400427  
C;Genetics:

A;Gene: ancl  
A;Intons: 37/3; 200/1; 247/1  
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C;Keywords: duplication; transmembrane protein  
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2; Length 298;  
Best Local Similarity 94.4%; Pred. No. 4.1e-125;  
Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
Db 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
Qy 61 IPKQGFSLFMRGNLANVIRFPQALNFAFKDKYKQFLGSDVRHQQPMRYFPGNLASG 120  
Db 61 IPKQGFSLFMRGNLANVIRFPQALNFAFKDKYKQFLGSDVRHQQPMRYFPGNLASG 120  
Qy 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 179  
Db 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 180  
Qy 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMIAQSVTAVALGVSYPDTRRRMM 239  
Db 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMIAQSVTAVALGVSYPDTRRRMM 240  
Qy 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 297  
Db 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 297

Db 241 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 298

# RESULT 3

ADP,ATP carrier protein T1 - mouse

N;Alternate names: adenine nucleotide carrier  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999  
C;Accession: S37210

R;Rajalace, C.; Coates, P.  
submitted to the EMBL data library, September 1993  
A;Reference number: S37210  
A;Accession: S37210

A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-298 <LAP>  
A;Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628  
C;Genetics:

A;Gene: Ancl  
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C;Keywords: duplication; transmembrane protein  
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2; Length 298;  
Best Local Similarity 94.0%; Pred. No. 7.6e-125;  
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
Db 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60  
Qy 61 IPKQGFSLFMRGNLANVIRFPQALNFAFKDKYKQFLGSDVRHQQPMRYFPGNLASG 120  
Db 61 IPKQGFSLFMRGNLANVIRFPQALNFAFKDKYKQFLGSDVRHQQPMRYFPGNLASG 120  
Qy 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 179  
Db 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 180  
Qy 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMIAQSVTAVALGVSYPDTRRRMM 239  
Db 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMIAQSVTAVALGVSYPDTRRRMM 240  
Qy 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 297  
Db 241 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 298

# RESULT 4

ADP,ATP carrier protein T1 - bovine

N;Alternate names: ADP/ATP translocase T1  
C;Species: Bos primigenius laurus (cattle)  
C;Date: 14-Nov-1983 #sequence\_revision 22-Jul-1994 #text\_change 22-Jun-1999  
C;Accession: A43646; A24822; A03181; A61343; S69369  
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.  
Biochemistry 28, 866-873, 1989

A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
A;Reference number: A43646; MUID:99229093; PMID:2540808  
A;Accession: A43646  
A;Molecule type: mRNA  
A;Residues: 1-298 <POW>

A;Cross-references: GB:A24102; NID:g529414; PIDN:AAA30768.1; PID:g529415  
R;Raamussen, U.B.; Mohlrad, H.  
Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual  
A;Reference number: A24822; MUID:86295775; PMID:3017341  
A;Accession: A24822  
A;Molecule type: mRNA  
A;Residues: 208-298 <RAS>

Qy 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 297  
Db 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKYV 297

A/Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631  
 R:Aquila, H.; Misra, D.; Eulitz, M.; Klingenberg, M.  
 H. Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982  
 A/Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria  
 A/Reference number: A03181; MUID:82186267; PMID:7076130  
 A/Accession: A03181  
 A/Molecule type: protein  
 A/Residues: 2-51, 'X', '53-70', 'X', '111-238 <AGU>  
 A/Note: residue 52 may be methyllysine  
 R:Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.  
 Biochim. Biophys. Acta 670, 176-180, 1981  
 A/Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria  
 A/Reference number: A61343; MUID:82046808; PMID:6271240  
 A/Accession: A61343  
 A/Molecule type: protein  
 A/Residues: 205-238 <BAB>  
 R:Oetmeier, W.; Masson, K.; Kalina, S.  
 Eur. J. Biochem. 227, 730-733, 1995  
 A/Title: [(3)H]-7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/ATP carrier  
 A/Reference number: S69369; MUID:95172058; PMID:7867632  
 A/Accession: S69369  
 A/Molecule type: protein  
 A/Residues: 49-63;154-168 <OET>  
 C/Comment: This protein is synthesized in the cytosol and transported into the mitochondria  
 C/Complex: homodimer  
 C/Function:  
 A/Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP generated by oxidative phosphorylation in the inner mitochondrial membrane  
 A/Note: located in the inner mitochondrial membrane  
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C/Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochondria; 110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>  
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>  
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACPI>  
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental  
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 93.9%; Score 1458.5; DB 1; Length 298;  
 Best Local Similarity 94.3%; Pred. No. 2.2e-114;  
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGDHMSFLDPLAGAAVAASKTAVAPIRVKKLLQVQHASQISAEKQYKGIIDCVR 60  
 Db 1 MSDQALSLDPLAGAAVAASKTAVAPIRVKKLLQVQHASQISAEKQYKGIIDCVR 60  
 QY 61 IPKQGLSTFRKGLAVIRFPQALNPAFKYKQLFLGVDNRHQPFMYFAGNTASG 120  
 Db 61 IPKQGLSTFRKGLAVIRFPQALNPAFKYKQLFLGVDNRHQPFMYFAGNTASG 120  
 QY 121 GAAGATSLCFYPLDPAFTRLAADVGR-RAOREFHGAGDCTIKLFFKSDGLRGVQGFNV 179  
 Db 121 GAAGATSLCFYPLDPAFTRLAADVGR-RAOREFHGAGDCTIKLFFKSDGLRGVQGFNV 180  
 QY 180 VQGIIRYRAAYFGVYDPAKGLDPPKXVHIFVSMIAQSYTAVAGLSYFDPYRRMM 239  
 Db 181 VQGIIRYRAAYFGVYDPAKGLDPPKXVHIFVSMIAQSYTAVAGLSYFDPYRRMM 240  
 QY 240 QSGRKADIMYTGTVDCMKRIADDEGAKAFKGMASVNLKMGAFVLYVDEIKKY 297  
 Db 241 QSGRKADIMYTGTVDCMKRIADDEGAKAFKGMASVNLKMGAFVLYVDEIKKY 298

RESULT 5  
 A29132  
 ADP/ATP carrier protein T2 - human  
 N/Alternate names: mitochondrial ADP/ATP translocase 2  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C/Accession: A29132; C28116  
 R:Bettini, R.; Ferrati, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.  
 J. Biol. Chem. 267, 4355-4359, 1992  
 A/Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated  
 A/Reference number: A29132; MUID:8716056; PMID:3031073  
 A/Accession: A29132

A/Molecule type: mRNA  
 A/Residues: 1-298 <BAT>  
 A/Cross-references: GB:002683; NID:g179246; PIDN:AAA35579.1; PID:g179247  
 R:Houldsworth, J.; Attardi, G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
 A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
 A/Reference number: A94197; MUID:88124845; PMID:2829183  
 A/Accession: C28116  
 A/Molecule type: mRNA  
 A/Residues: 47-65, 'G', 67-110, 'U', 112-161, 'G', 163-298 <HOU>  
 A/Cross-references: GB:003591; NID:g339720; PIDN:AAA36749.1; PID:g339721  
 A/Experimental source: clone pAT3  
 C/Genetics:  
 A/Gene: GDB:AMT2; T3; 2P1  
 A/Cross-references: GDB:125190; OMIM:300150  
 A/Map position: Xq13-Xq26  
 A/Note: there may be some confusion in the assignment of sequences for GDB:AMT2 and GDB:  
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C/Keywords: duplication; homodimer; mitochondria; transmembrane protein  
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>  
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>  
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 89.6%; Score 1391.5; DB 1; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 2.5e-118;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLDPLAGAAVAASKTAVAPIRVKKLLQVQHASQISAEKQYKGIIDCVR 60  
 Db 1 MTDALSLDPLAGAAVAASKTAVAPIRVKKLLQVQHASQISAEKQYKGIIDCVR 60  
 QY 61 IPKQGLSTFRKGLAVIRFPQALNPAFKYKQLFLGVDNRHQPFMYFAGNTASG 120  
 Db 61 IPKQGLSTFRKGLAVIRFPQALNPAFKYKQLFLGVDNRHQPFMYFAGNTASG 120  
 QY 121 GAAGATSLCFYPLDPAFTRLAADVGR-RAOREFHGAGDCTIKLFFKSDGLRGVQGFNV 179  
 Db 121 GAAGATSLCFYPLDPAFTRLAADVGR-RAOREFHGAGDCTIKLFFKSDGLRGVQGFNV 180  
 QY 180 VQGIIRYRAAYFGVYDPAKGLDPPKXVHIFVSMIAQSYTAVAGLSYFDPYRRMM 239  
 Db 181 VQGIIRYRAAYFGVYDPAKGLDPPKXVHIFVSMIAQSYTAVAGLSYFDPYRRMM 240  
 QY 240 QSGRKADIMYTGTVDCMKRIADDEGAKAFKGMASVNLKMGAFVLYVDEIKKY 296  
 Db 241 QSGRKADIMYTGTVDCMKRIADDEGAKAFKGMASVNLKMGAFVLYVDEIKKY 297

RESULT 6  
 S03894  
 ADP/ATP carrier protein T3 - human  
 N/Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP/ATP  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C/Accession: S03894; B28116  
 R:Cozens, A.L.; Rumewick, M.J.; Walker, J.E.  
 J. Mol. Biol. 206, 261-280, 1989  
 A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr.  
 A/Reference number: S03893; MUID:89236396; PMID:2541251  
 A/Accession: S03894  
 A/Status: not compared with conceptual translation  
 A/Molecule type: DNA  
 A/Residues: 1-298 <COZ>  
 R:Houldsworth, J.; Attardi, G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
 A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
 A/Reference number: A94197; MUID:88124845; PMID:2829183  
 A/Accession: B28116  
 A/Molecule type: mRNA  
 A/Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>  
 A/Cross-references: GB:003592; NID:g339722; PIDN:AAA36750.1; PID:g339723  
 A/Experimental source: liver  
 C/Genetics:

A;Gene: GDB:ANT3; ANT3Y  
 A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000  
 A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3  
 A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:  
 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
 C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F;2-298/Product: ADP,ATP carrier protein status predicted <MAT>  
 F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
 F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
 F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 89.2%; Score 1385.5; DB 1; Length 298;  
 Best Local Similarity 87.2%; Pred. No. 8.8e-118;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
 DB 1 MTEQALISFADPLAGGIAAISKTAIVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREPHGLGDCIYIKFKSDGLRGLYOGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFAFRTLAADVGRSGTEREFGJGDLVKTYSKDGKGLYOGFSVS 180  
 QY 180 VQGIITIRAAVFGVYDPAKGLPDPKXVHIFVSMIAQSVTAVALGLSYFPDTRRRMM 239  
 DB 181 VQGIITIRAAVFGVYDPAKGLPDPKXVHIFVSMIAQSVTAVALGLSYFPDTRRRMM 240  
 QY 240 QSGRKGADIMYTGTVDCMRKIADDEGAKAFPKGAMSVNLKMGAFVLVYDEIKKY 297  
 DB 241 QSGRKGADIMYTGTVDCMRKIFRDEGKAFPKGAMSVNLKMGAFVLVYDEIKKY 298

## RESULT 7

B43646  
 ADP,ATP carrier protein T2 - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 20-Aug-1999  
 C;Accession: B43646  
 R;Powell, S.U.; Medd, S.M.; Runswick, M.J.; Walker, J.E.  
 Biochemistry 28, 866-873, 1989  
 A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
 A;Reference number: A43646; PMID:89229093; PMID:2540808  
 A;Accession: B43646  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-298 <POM>  
 A;Cross-references: GB:M424103; NID:9529416; PIDN:AAA30769.1; PID:9529417  
 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
 C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
 F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
 F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.9%; Score 1380.5; DB 2; Length 298;  
 Best Local Similarity 86.9%; Pred. No. 2.5e-117;  
 Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;  
 QY 1 MGDHANSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
 DB 1 MTEQALISFADPLAGGIAAISKTAIVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREPHGLGDCIYIKFKSDGLRGLYOGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFAFRTLAADVGRSGTEREFGJGDLVKTYSKDGKGLYOGFNVS 180

QY 180 VQGIITIRAAVFGVYDPAKGLPDPKXVHIFVSMIAQSVTAVALGLSYFPDTRRRMM 239  
 DB 181 VQGIITIRAAVFGVYDPAKGLPDPKXVHIFVSMIAQSVTAVALGLSYFPDTRRRMM 240  
 QY 240 QSGRKGADIMYTGTVDCMRKIADDEGAKAFPKGAMSVNLKMGAFVLVYDEIKKY 297  
 DB 241 QSGRKGADIMYTGTVDCMRKILNDEGAKAFPKGAMSVNLKMGAFVLVYDEIKKY 298

## RESULT 8

S31814  
 ADP,ATP carrier protein T2 - mouse  
 N;Alternate names: adenine nucleotide translocase  
 C;Species: Mus musculus (house mouse)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Apr-1998  
 C;Accession: S31814  
 R;Coates, P.; Laplace, C.  
 submitted to the EMBL data library, January 1993  
 A;Reference number: S31814  
 A;Accession: S31814  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-298 <COS>  
 A;Cross-references: EMBL:X70847  
 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
 C;Keywords: duplication; transmembrane protein  
 F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
 F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
 F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.1%; Score 1368.5; DB 2; Length 298;  
 Best Local Similarity 87.2%; Pred. No. 3e-116;  
 Matches 259; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
 DB 1 MTDNANSFADPLAGGIAAISKTAIVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREPHGLGDCIYIKFKSDGLRGLYOGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFAFRTLAADVGRSGTEREFGJGDLVKTYSKDGKGLYOGFNVS 180  
 QY 180 VQGIITIRAAVFGVYDPAKGLPDPKXVHIFVSMIAQSVTAVALGLSYFPDTRRRMM 239  
 DB 181 VQGIITIRAAVFGVYDPAKGLPDPKXVHIFVSMIAQSVTAVALGLSYFPDTRRRMM 240  
 QY 240 QSGRKGADIMYTGTVDCMRKIADDEGAKAFPKGAMSVNLKMGAFVLVYDEIKKY 296  
 DB 241 QSGRKGADIMYTGTVDCMRKIADDEGAKAFPKGAMSVNLKMGAFVLVYDEIKKY 297

## RESULT 9

S31935  
 ADP,ATP carrier protein - African malaria mosquito  
 C;Species: Anopheles gambiae (African malaria mosquito)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: S31935; S31936  
 R;Beard, C.B.; Crews-Owen, A.E.; Collins, F.H.  
 submitted to the EMBL data library, February 1993  
 A;Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.  
 A;Reference number: S31935  
 A;Accession: S31935  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-301 <BEA>  
 A;Cross-references: EMBL:Z21814; EMBL:Z21815  
 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
 C;Keywords: duplication; transmembrane protein  
 F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F;209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 73.6%; Score 1142.5; DB 1; Length 301;  
Best Local Similarity 76.2%; Pred. No. 8.8e-96;  
Matches 221; Conservative 26; Mismatches 42; Indels 1; Gaps 1;

Qy 6 WSPFLDAGAVAAVSKTAVPIERVKLLQVQHASKOISAEKQYGIIDCVRIPEQ 65  
Db 8 YGPAKDLAAGISAAVSKTAVPIERVKLLQVQHASKOISAEKQYGIIDCVRIPEQ 67

Qy 66 GFLSPWRGNLANVIRYPTQALNPAFKDKYKOLFVGVDRHKQFWRYPAGNLTASGAAGA 125  
Db 68 GIGAFCCGNLANVIRYPTQALNPAFKDKYKOLFVGVDRHKQFWRYPAGNLTASGAAGA 127

Qy 126 TSLCFVYPLDPARTRLAADVGRRA-QREFHGLGCIITIKFSDDLKGLYOGFVNSVGGIIT 184  
Db 128 TSLCFVYPLDPARTRLAADVGRRA-QREFHGLGCIITIKFSDDLKGLYOGFVNSVGGIIT 187

Qy 185 IYRAAYGVYDTAKGMLPDPKGVHIFVSWMTAQSVAAGLSYPTVRRRMMQSGRK 244  
Db 188 IYRAAYGVYDTAKGMLPDPKGVHIFVSWMTAQSVAAGLSYPTVRRRMMQSGRK 247

Qy 245 GADIMYTGTVDCWRKIADEGAKAFPKGMSNVLRGMGAFVLYLDEIK 294  
Db 248 KSEVMTKNTLDCAVVKIKNEGMSAMFKGALSIVFRGTGALVLAIDEIKFI 297

# RESULT 10

T25850  
hypothetical protein T01B11.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C/Accession: T25850  
R/Gelbel, C.; Stelleyes, L.  
submitted to the EMBL Data Library, December 1996

A/Description: The sequence of C. elegans cosmid T01B11.  
A/Reference number: Z20099

A/Accession: T25850  
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
A/Residues: 1-313 <GBI>

A/Cross-references: EMBL:U09031; PIDN:AA38001.1; GSPDB:GN00022; CESP:T01B11.4  
A/Experimental source: strain Bristol N2; clone T01B11

C/Genetic8:  
A/Map position: 4  
A/Intons: 4/1; 191/2

C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1045.5; DB 2; Length 313;  
Best Local Similarity 69.8%; Pred. No. 5.6e-87;  
Matches 203; Conservative 36; Mismatches 49; Indels 3; Gaps 2;

Qy 8 FLKDFLAGAVAAVSKTAVPIERVKLLQVQHASKOISAEKQYGIIDCVRIPEQ 67  
Db 25 FLIDLASGTAAGTAASKTAVPIERVKLLQVQHASKOISAEKQYGIIDCVRIPEQ 84

Qy 68 LSPWRGNLANVIRYPTQALNPAFKDKYKOLFVGVDRHKQFWRYPAGNLTASGAAGA 127  
Db 85 AALWRGNLANVIRYPTQALNPAFKDKYKOLFVGVDRHKQFWRYPAGNLTASGAAGA 144

Qy 128 LCFVYPLDPARTRLAADVGRRA-QREFHGLGCIITIKFSDDLKGLYOGFVNSVGGIIT 187  
Db 145 LCFVYPLDPARTRLAADVGRRA-QREFHGLGCIITIKFSDDLKGLYOGFVNSVGGIIT 204

Qy 188 AAYGVYDTAKGMLPDPKGVHIFVSWMTAQSVAAGLSYPTVRRRMMQSGRK 246  
Db 205 AAYGVYDTAKGMLPDPKGVHIFVSWMTAQSVAAGLSYPTVRRRMMQSGRK 262

Qy 247 DIMYTGTVDCWRKIADEGAKAFPKGMSNVLRGMGAFVLYLDEIKYV 297  
Db 263 DVLYKNTLDCAVVKIKNEGMSAMFKGALSIVFRGTGALVLAIDEIKFI 313

## RESULT 11

T23207  
hypothetical protein K01H12.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C/Accession: T23207  
R/McMurray, A.  
submitted to the EMBL Data Library, December 1995

A/Reference number: Z19707  
A/Accession: T23207

A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA

A/Residues: 1-313 <Wtl>  
A/Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2

A/Experimental source: clone K01H12  
C/Genetic8:

A/Map position: 4  
A/Intons: 4/1; 191/2

C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.2%; Score 1043.5; DB 2; Length 313;  
Best Local Similarity 69.4%; Pred. No. 8.5e-87;  
Matches 202; Conservative 37; Mismatches 49; Indels 3; Gaps 2;

Qy 8 FLKDFLAGAVAAVSKTAVPIERVKLLQVQHASKOISAEKQYGIIDCVRIPEQ 67  
Db 25 FLIDLASGTAAGTAASKTAVPIERVKLLQVQHASKOISAEKQYGIIDCVRIPEQ 84

Qy 68 LSPWRGNLANVIRYPTQALNPAFKDKYKOLFVGVDRHKQFWRYPAGNLTASGAAGA 127  
Db 85 AALWRGNLANVIRYPTQALNPAFKDKYKOLFVGVDRHKQFWRYPAGNLTASGAAGA 144

Qy 128 LCFVYPLDPARTRLAADVGRRA-QREFHGLGCIITIKFSDDLKGLYOGFVNSVGGIIT 187  
Db 145 LCFVYPLDPARTRLAADVGRRA-QREFHGLGCIITIKFSDDLKGLYOGFVNSVGGIIT 204

Qy 188 AAYGVYDTAKGMLPDPKGVHIFVSWMTAQSVAAGLSYPTVRRRMMQSGRK 246  
Db 205 AAYGVYDTAKGMLPDPKGVHIFVSWMTAQSVAAGLSYPTVRRRMMQSGRK 262

Qy 247 DIMYTGTVDCWRKIADEGAKAFPKGMSNVLRGMGAFVLYLDEIKYV 297  
Db 263 DVLYKNTLDCAVVKIKNEGMSAMFKGALSIVFRGTGALVLAIDEIKFI 313

## RESULT 12

T25371  
hypothetical protein T27B9.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C/Accession: T25371  
R/Lloyd, C.

submitted to the EMBL Data Library, November 1996  
A/Reference number: Z20024

A/Accession: T25371  
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
A/Residues: 1-300 <Wtl>

A/Cross-references: EMBL:Z62059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27B9.1  
A/Experimental source: clone T27B9

C/Genetic8:  
A/Map position: 3  
A/Intons: 20/1; 41/3; 115/2

C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 66.8%; Score 1037.5; DB 2; Length 300;  
Best Local Similarity 69.1%; Pred. No. 2.8e-86;  
Matches 201; Conservative 38; Mismatches 49; Indels 3; Gaps 2;

QY 8 FLKDFLAGAANAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKEGF 67  
 DB 12 FLIDIASGATAAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKEGF 71  
 QY 68 LSPFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAGATS 127  
 DB 72 AAFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAGATS 131  
 QY 128 LCFVYPLDFPARTLADYVGRRAQREPHGLGDCIIRKIFPSDGLRGLYOGFNNVSGGIIIR 187  
 DB 132 LCFVYPLDFPARTLADYVGRRAQREPHGLGDCIIRKIFPSDGLRGLYOGFNNVSGGIIIR 191  
 QY 188 AAFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAGATS 246  
 DB 192 AAFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAGATS 249  
 QY 247 DIMYGTVDGCRKRIADGAKAFKFGANSNVLRGMGAFVLTLYDEIKKYV 297  
 DB 250 DIMYGTVDGCRKRIADGAKAFKFGANSNVLRGMGAFVLTLYDEIKKYV 300

## RESULT 13

hypochemical protein W02D3.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jan-2000  
 C:Accession: T15206  
 R:Le, T.; Weinstein, L.; Rifkin, L.  
 submitted to the EMBL Data Library, May 1997  
 A:Description: The sequence of C. elegans cosmid W02D3.  
 A:Reference number: Z18308  
 A:Accession: T15206  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-300 <LEFT>  
 A:Cross-references: EMBL:AF003141; NID:G2088732; PID:G2088738; PIDN:AA854179.1; GSPDB:GN  
 A:Experimental source: strain Bristol N2; clone W02D3  
 C:Genetics:  
 A:Gene: CESP:W02D3.6  
 A:Map position: 1  
 C:Superfamily: ADP, ATP carrier protein repeat homology <ACR>  
 F:9-103/Domain: ADP, ATP carrier protein repeat homology <ACR>

Query Match 64.7%; Score 1005.5; DB 2; Length 300;  
 Best Local Similarity 66.0%; Pred. No. 2.2e-83;  
 Matches 192; Conservative 40; Mismatches 56; Indels 3; Gaps 2;  
 QY 8 FLKDFLAGAANAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKEGF 67  
 DB 12 FLIDIASGATAAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKEGF 71  
 QY 68 LSPFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAGATS 127  
 DB 72 AAFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAGATS 131  
 QY 128 LCFVYPLDFPARTLADYVGRRAQREPHGLGDCIIRKIFPSDGLRGLYOGFNNVSGGIIIR 187  
 DB 132 LCFVYPLDFPARTLADYVGRRAQREPHGLGDCIIRKIFPSDGLRGLYOGFNNVSGGIIIR 191  
 QY 188 AAFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAGATS 246  
 DB 192 AAFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAGATS 249  
 QY 247 DIMYGTVDGCRKRIADGAKAFKFGANSNVLRGMGAFVLTLYDEIKKYV 297  
 DB 250 DIMYGTVDGCRKRIADGAKAFKFGANSNVLRGMGAFVLTLYDEIKKYV 300

RESULT 14  
 A41677  
 ADP, ATP carrier protein - Chlorella kessleri  
 C:Species: Chlorella kessleri  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999

C:Accession: A41677  
 R:Highgate, C.; Sauer, N.; Tanner, W.  
 J. Biol. Chem. 266, 24044-24047, 1991  
 A:Title: Glucose increases the expression of the ATP/ADP translocator and the glyceralde  
 A:Reference number: A41677; MUID:92084708; PMID:1748677  
 A:Accession: A41677  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-339 <HLL>  
 A:Cross-references: GB:M76669; NID:G516596; PIDN:AAA33027.1; PID:G516597  
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F:138-134/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
 F:144-235/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
 F:241-339/Domain: ADP, ATP carrier protein repeat homology <ACPI>

Query Match 62.7%; Score 973.5; DB 2; Length 339;  
 Best Local Similarity 65.3%; Pred. No. 2e-80;  
 Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;  
 QY 7 SFLKDFLAGAANAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKE 64  
 DB 40 AFDKDLASGATAAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKE 99  
 QY 65 LSPFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAG 124  
 DB 100 QGVASFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAG 158  
 QY 125 AFSICFVYPLDFPARTLADYVGRRAQREPHGLGDCIIRKIFPSDGLRGLYOGFNNVSGGII 184  
 DB 159 AGSLIYPLDFPARTLADYVGRRAQREPHGLGDCIIRKIFPSDGLRGLYOGFNNVSGGII 218  
 QY 185 IYRAAYRGVYDTAKGML-PDPKRVHIFVSMIAQSVTAVALSLSPPTVRRRMMQSGR 243  
 DB 219 YVRGAYRGVYDTAKGML-PDPKRVHIFVSMIAQSVTAVALSLSPPTVRRRMMQSGR 276  
 QY 244 KGAIDMTGTVDCRKRKIAADGAKAFKFGANSNVLRGMGAFVLTLYDEIKKYV 297  
 DB 277 -GGRQYNGTIDGCRKRIADGAKAFKFGANSNVLRGMGAFVLTLYDEIKKYV 329

## RESULT 15

SS1132  
 ADP, ATP carrier protein - malaria parasite (Plasmodium falciparum)  
 N:Alternate names: ADP/ATP transporter  
 C:Species: Plasmodium falciparum  
 C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jun-2000  
 C:Accession: S68993; SS1132  
 R:Haftin, I.; Daureguberry, G.  
 Eur. J. Biochem. 228, 86-91, 1995  
 A:Title: Molecular characterization of the ADP/ATP-transporter cDNA from the human malar  
 A:Reference number: S68993; MUID:95188918; PMID:7683016  
 A:Accession: S68993  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-301 <HAT>  
 A:Cross-references: EMBL:X83551; NID:G623334; PIDN:CAA58541.1; PID:G623335  
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C:Keywords: duplication; transmembrane protein  
 F:6-102/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
 F:112-203/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
 F:209-301/Domain: ADP, ATP carrier protein repeat homology <ACPI>

Query Match 58.2%; Score 904.5; DB 2; Length 301;  
 Best Local Similarity 58.3%; Pred. No. 3.1e-74;  
 Matches 172; Conservative 46; Mismatches 70; Indels 5; Gaps 4;  
 QY 7 SFLKDFLAGAANAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKE 64  
 DB 8 NFADFLMGISAAISKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKE 67  
 QY 65 QGFLSPFRGNLANVIRYPTQALNFAFDKQYKQLFLGVDNRHKKQFWRFPAGNLASGGAAG 124

Db 68 QGVLSLMRGVNAVIRYFPTQAFNFAKDYFKNIF-PRYDONTDSKFCVNIISGATAG 126  
 QY 125 ATSLCFYVPLDFAFTRPLADYGRRAQREHGLGDCIIFKESDGLRGYOGFNYSVQGI 184  
 Db 127 AISTLIIVPLDFARIRLASDYGKGRQFTGLFDCLAKIVKQTGLSLYSFGVSVTGII 186  
 QY 185 IYRAAYFGVYDTAKGML-PDPKNVHIFVSMIAOSVTAVAGILSYFEDTVRRMMOSGR 243  
 Db 187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKMVAOSVTIAGLISYFPDTVRRMMMSGR 246  
 QY 244 KG-ADIMYTGTVDCWRKIADKDGAKAFPKGAMSVNLRGMGAFVLVYDEIKKTV 297  
 Db 247 KGKEEIOYKNTIDCWIKILRNKGFGFKGAMNAVIRGAGALVLFYDELOKLI 301

Search completed: December 18, 2003, 12:44:04  
 Job time : 15.3012 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:16:16 ; Search time 8.31467 Seconds  
(without alignments)  
1679.794 Million cell updates/sec

Title: US-09-811-131-31  
1553

Sequence: 1 MGDHMSFLKDFLAGAVAA.....LRMGGAFLVLYDEIKKYV 297

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.4	298	1	ADT1_HUMAN
2	1466.5	94.4	298	1	ADT1_HUMAN
3	1463.5	94.2	298	1	ADT1_MOUSE
4	1453.5	93.6	297	1	ADT1_BOVIN
5	1408.5	90.7	298	1	ADT2_MOUSE
6	1407.5	90.6	298	1	ADT2_MOUSE
7	1398.5	90.1	298	1	ADT2_HUMAN
8	1385.5	89.2	298	1	ADT3_HUMAN
9	1380.5	88.9	298	1	ADT3_BOVIN
10	1241	79.9	299	1	ADT_DROME
11	1162.5	74.9	301	1	ADT_ANOGA
12	973.5	62.7	339	1	ADT_CHLKE
13	770.5	49.6	308	1	ADT_CHLKE
14	756.5	48.7	387	1	ADT1_MAIZE
15	752.5	48.5	386	1	ADT1_MAIZE
16	752.5	48.5	386	1	ADT1_MAIZE
17	751.5	48.4	382	1	ADT1_GOSHI
18	751.5	48.4	382	1	ADT1_GOSHI
19	746	48.0	381	1	ADT1_MAIZE
20	744.5	47.9	386	1	ADT1_SOLTU
21	742.5	47.8	331	1	ADT1_WHEAT
22	740	47.6	386	1	ADT2_SOLTU
23	736	47.4	307	1	ADT3_YEAST
24	734	47.3	318	1	ADT2_YEAST
25	733.5	47.1	313	1	ADT1_NEUCR
26	731	47.1	385	1	ADT2_ARATH
27	729	46.9	305	1	ADT_KUTLA
28	728.5	46.9	331	1	ADT2_WHEAT
29	718.5	46.3	309	1	ADT1_YEAST
30	718.5	46.3	309	1	ADT1_YEAST
31	700.5	19.5	678	1	CMC1_HUMAN
32	296.5	19.1	565	1	CMC3_BOVIN
33	296.5	19.1	702	1	CMC1_CABEL

34	296	19.1	588	1	CMC2_CABEL
35	295	19.0	322	1	GDC_RAT
36	292.5	18.8	307	1	ODC2_YEAST
37	292	18.8	332	1	GDC_HUMAN
38	291	18.7	675	1	CMC2_HUMAN
39	280	18.0	315	1	MFT_HUMAN
40	279.5	18.0	676	1	CMC2_MOUSE
41	270.5	17.4	315	1	SA18_HUMAN
42	267.5	17.2	325	1	UCP5_MOUSE
43	266.5	17.2	310	1	ODC1_YEAST
44	265.5	17.1	325	1	UCP5_HUMAN
45	263.5	17.0	695	1	CMC1_DROME

## ALIGNMENTS

RESULT 1	ID	ADT1_HUMAN	STANDARD	PRT	298 AA
AC	P12235				
DT	01-OCT-1989	(Rel. 12, Created)			
DT	01-NOV-1990	(Rel. 16, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).				
GN	SLC25A4 OR ANT1				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.				
OX	NCBI_TaxID=9606				
RN	[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=89236396; PubMed=2541251;				
RX	Cozens A.L., Runswick M.J., Walker J.E.;				
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";				
RL	J. Mol. Biol. 206:261-280(1989).				
RN	[2]	SEQUENCE FROM N.A.			
RP	MEDLINE=89340499; PubMed=2547778;				
RX	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;				
RT	"A human muscle adenine nucleotide translocator gene has four exons, and is located on chromosome 4, and is differentially expressed.";				
RL	J. Biol. Chem. 264:13998-14004(1989).				
RN	[3]	SEQUENCE FROM N.A.			
RP	MEDLINE=88041149; PubMed=2823266;				
RX	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;				
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).				
RN	[4]	SEQUENCE FROM N.A.			
RP	TISSUE=Eye;				
RC	MEDLINE=22388257; PubMed=12477932;				
RX	Strauberg R.L., Fetingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [5]  
 RN SEQUENCE OF 1-37 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88124845; PubMed=2829183;  
 RA Houldsworth J., Altardi G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 RT level in adult human liver.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).  
 RN [6]  
 RN VARIANTS PEO PRO-114 AND MET-289.  
 RX MEDLINE=20385067; PubMed=10926541;  
 RA Karkonen J., Junesius J.K., Tirant V., Kyttala A., Zeviani M.,  
 RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;  
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";  
 RL Science 289:782-785 (2000).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant  
 CC progressive external ophthalmoplegia with various mitochondrial  
 CC DNA deletions (PEO). Patients with PEO have mitochondrial  
 CC myopathy, progressive external ophthalmoplegia, and other  
 CC abnormalities associated with multiple different deletions of  
 CC mitochondrial DNA.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, J02966; AAA61223.1; -;  
 DR EMBL, J03593; AAA36751.1; -;  
 DR EMBL, J04982; AAA51736.1; -;  
 DR EMBL, BC008664; AAH08664.1; -;  
 DR PIR, A44778; A44778;  
 DR Genew, HGNC:10990; SLC25A4.  
 DR MIM, 103220; -;  
 DR GO, GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO, GO:0005739; C:mitochondrion; TAS.  
 DR GO, GO:0015207; F:adenine transporter activity; TAS.  
 DR GO, GO:0006091; F:energy pathways; TAS.  
 DR GO, GO:0000002; F:mitochondrial genome maintenance; TAS.  
 DR GO, GO:0006832; F:small molecule transport; TAS.  
 DR InterPro, IPR002067; Mlt carrier.  
 DR InterPro, IPR002030; Mlt uncoupling.  
 DR InterPro, IPR001993; Mito carrier.  
 DR Pfam, PF00153; mito\_carr; 3.  
 DR PRINTS, PRO0926; MITOCARRIER.  
 DR PRINTS, PRO0784; MTNDCOUPLING.  
 DR PROSITE, PS00215; MITOCH CARRIER; 3.  
 KW Mitochondrion, Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family; Disease mutation.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 110 1.  
 FT REPEAT 111 208 2.

FT REPEAT 209 298 3.  
 FT VARIANT 114 114 A->P (IN PEO).  
 FT VARIANT 289 289 /FTID=VAR 012111.  
 FT VARIANT 289 289 V->M (IN PEO).  
 FT VARIANT 289 289 /FTID=VAR 012112.  
 FT CONFLICT 16 16 G->A (IN REF. 3).  
 FT CONFLICT 147 149 KGA->RR (IN REF. 3).  
 FT CONFLICT 227 227 V->L (IN REF. 3).  
 SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAEC4E7CFFB CRC64;  
 Query Match 98.3%; Score 1526.5; DB 1; Length 298;  
 Best Local Similarity 98.3%; Pred. No. 2e-129;  
 Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
 QY 1 MGDHMSFLKDFLAGAFAAASKTAVAFIEKVKLLQVQHASKQISAEKQYKGIIDCYR 60  
 DB 1 MGDHMSFLKDFLAGAFAAASKTAVAFIEKVKLLQVQHASKQISAEKQYKGIIDCYR 60  
 QY 61 IPKEGFLSPWRGNLANVIRFPQALNPAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120  
 DB 61 IPKEGFLSPWRGNLANVIRFPQALNPAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120  
 QY 121 GAAGATSLCFYYPIDPAPTRIAADVGR-RAQREFHGLDCTIKTIPKSDGLKGLYOGFNV 179  
 DB 121 GAAGATSLCFYYPIDPAPTRIAADVGR-RAQREFHGLDCTIKTIPKSDGLKGLYOGFNV 180  
 QY 180 VGGIITVYAAFGYDTAKGMLPDPKNVHIFVSWMIAGSVTAAGLSYPEDTVRRMM 239  
 DB 181 VGGIITVYAAFGYDTAKGMLPDPKNVHIFVSWMIAGSVTAAGLSYPEDTVRRMM 240  
 QY 240 QSGRKADIMTGVNDCKRIAKDEGAKAFKGMNSVLRMGAGFVLYLDEIKKY 297  
 DB 241 QSGRKADIMTGVNDCKRIAKDEGAKAFKGMNSVLRMGAGFVLYLDEIKKY 298  
 RESULT 2  
 ADT1 RAT STANDARD, PRT; 298 AA.  
 ID ADT1\_RAT  
 AC Q05962;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP  
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
 GN SLC25A4 OR ANT1.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;  
 RX MEDLINE=94002161; PubMed=8399300;  
 RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;  
 RT "Isolation and characterization of cDNA clones and a genomic clone  
 RT encoding rat mitochondrial adenine nucleotide translocator.";  
 RL Biochem. Biophys. Acta 1152:192-196 (1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER  
 CC EXTENT, IN BRAIN AND KIDNEY.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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or send an email to [license@eb-sib.ch](mailto:license@eb-sib.ch).

CC EMBL; X61667; CA43842.1; -  
 DR EMBL; D12770; BAA02237.1; -  
 DR PIR; I60173; I60173.  
 DR InterPro; IPR002067; Mlt carrier.  
 DR InterPro; IPR002030; Mlt uncoupling.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR Pfam; PF00153; mito\_carr; 3\_  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUOCOUPLING.  
 DR PROSITE; PS00215; MITOCH CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 110 1.  
 FT REPEAT 111 208 2.  
 FT REPEAT 209 298 3.  
 SQ SEQUENCE 298 AA; 32389 MM; 66704FF78C6BC320 CRC64;  
 Query Match 94.4%; Score 1466.5; DB 1; Length 298;  
 Best Local Similarity 94.3%; Pred. No. 4.7e-124;  
 Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHAFSLKDFLAGAVALAAAKTAAPVPIERKILLQVQASKOISAEKQYGIIDCVR 60  
 Db 1 MGDALFLKDFLAGAVALAAAKTAAPVPIERKILLQVQASKOISAEKQYGIIDCVR 60  
 QY 61 IPKQGLSFWRKGLAVIRFPQALNFAFKDKYKQLFLGCGVDRHQPMRYFAGNTASG 120  
 Db 61 IPKQGLSFWRKGLAVIRFPQALNFAFKDKYKQLFLGCGVDRHQPMRYFAGNTASG 120  
 QY 121 GAAAGTSLCFYPLDPAPTRIAADVGR-RAGREFHSGDCLIKFKSDGLGLYQGFNS 179  
 Db 121 GAAAGTSLCFYPLDPAPTRIAADVGR-RAGREFHSGDCLIKFKSDGLGLYQGFNS 180  
 QY 180 VQGIITRAAFYGYDTAKGLPDPKVVHIFVSMIAQSVTAVALGLSYPPDYRRMM 239  
 Db 181 VQGIITRAAFYGYDTAKGLPDPKVVHIFVSMIAQSVTAVALGLSYPPDYRRMM 240  
 QY 240 QSGRKGADIMTGTVDCKRIAKDEGAKAFKGMASVLRGMGAPVLYLYDEIKKYV 297  
 Db 241 QSGRKGADIMTGTVDCKRIAKDEGAKAFKGMASVLRGMGAPVLYLYDEIKKYV 298

RESULT 3  
 ADT1\_MOUSE STANDARD; PRT; 298 AA.  
 ID ADT1\_MOUSE  
 AC P48962; O62164;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).  
 GN SLC25A4 OR ANT1 OR ANCI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=97059403; PubMed=8903724;  
 RA Ellisen J.W., Li X., Francke U., Shapiro L.J.;  
 RT "Rapid evolution of human pseudautosomal genes and their mouse homologs."  
 RL Mamm. Genome 7:25-30(1996).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Muscle;  
 RA Laplace C., Costet P.;  
 RL Submitted (SSP-1993) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Levy S.B., Chen Y.-S., Graham B.H., Wallace D.C.;  
 RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bye;  
 RX MEDLINE=23388257; PubMed=12477932;  
 RA Straubner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalak U., Smalls D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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CC EMBL; U27315; AAC52837.1; -  
 DR EMBL; X74510; CA52616.1; -  
 DR EMBL; AP240002; AAF64470.1; -  
 DR EMBL; BC003791; AAH03791.1; -  
 DR EMBL; BC026925; AAH26925.1; -  
 DR PIR; S37210; S37210.  
 DR MGD; MGI:1353495; SLC25A4.  
 DR InterPro; IPR002067; Mlt carrier.  
 DR InterPro; IPR002030; Mlt uncoupling.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR Pfam; PF00153; mito\_carr; 3\_  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUOCOUPLING.  
 DR PROSITE; PS00215; MITOCH CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 110 1.

FT	REPEAT	111	208	2	
FT	CONFLECT	136	136	F -> L (IN REF. 1).	
SO	SEQUENCE	298 AA;	32904 MW;	3A849FEAB0981462 CRC64;	
Query Match					
Best Local Similarity		94.2%;		Score 1463.5; DB 1; Length 298;	
Matches 280;		Conservative 10;		Pred. No. 8.7e-124;	
		Mismatch 7;		Indels 1; Gaps 1	
OY	1	MGDHAWSFLKDFLAGA	VAANAASKTA	VAPIERYKLLQVQHASKQISAEKQYKGIIDCVR 60	
DB	1	MGDQSLFLKDFLAGIA	AAVASKTA	VAPIERYKLLQVQHASKQISAEKQYKGIIDCVR 60	
OY	61	IPKEGFLSPFRGNLAN	YTRYPPQALNPA	FFDKTKQLFLGVGDVHHKQFWRFPAGNLASG 120	
DB	61	IPKEGFLSPFRGNLAN	YTRYPPQALNPA	FFDKTKQLFLGVGDVHHKQFWRFPAGNLASG 120	
OY	121	GAAGATSCFVYPLD	FARTRLAADYGR	-RAOREPFGLDGDCIKIKFSPDGLRGLYQGFNV 179	
DB	121	GAAGATSCFVYPLD	FARTRLAADYGR	-RAOREPFGLDGDCIKIKFSPDGLRGLYQGFNV 180	
OY	180	VGGIITRYAAAYGVY	DYAKGMLPDEK	NVHIFVSMNIAOSVTA	VAGLLSYFPDVRMM 239
DB	181	VGGIITRYAAAYGVY	DYAKGMLPDEK	NVHIFVSMNIAOSVTA	VAGLLSYFPDVRMM 240
OY	240	QSGRGADIMVTGT	YDWCARKIAKDG	KAKAFPGGANSNLR	KGGAFLVLYDEIKKYV 297
DB	241	QSGRGADIMVTGT	YDWCARKIAKDG	GANAVAFPGGANSNLR	KGGAFLVLYDEIKKYV 298
RESULT 4					
ADT1	BOVIN	STANDARD;	PRT;	297 AA.	
ID	ADT1_BOVIN	P02722;			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1993	(Rel. 26, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)				
DB	(Adenine nucleotide translocator 1) (ANT 1).				
GN	SLC25A4 OR ANT1.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89229093; PubMed=2540808;				
RA	Powell S.J., Medd S.M., Runswick M.J., Walker J.E.,				
RT	"Two bovine genes for mitochondrial ADP/ATP translocase expressed				
RT	differences in various tissues.";				
RL	Biochemistry 28:866-873(1989).				
RP	SEQUENCE.				
RX	MEDLINE=82188267; PubMed=7076130;				
RA	Aquila H., Misra D., Eulitz M., Klingenberg M.,				
RT	"Complete amino acid sequence of the ADP/ATP carrier from beef heart				
RT	mitochondria.";				
RL	Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).				
RN	[3]				
RP	SEQUENCE OF 207-297 FROM N.A.				
RX	MEDLINE=86295775; PubMed=3017341;				
RA	Raemussen U.B., Wohlrab H.,				
RT	"Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and				
RT	an unusually short 3'-noncoding sequence.";				
RL	Biochem. Biophys. Res. Commun. 133:850-857(1986).				
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE				
CC	MITOCHONDRIAL INNER MEMBRANE.				
CC	-1- SUBUNIT: Homodimer.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial				
CC	inner membrane.				
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.				
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.				

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DR EMBL; M13783; AAA30363.1; -.
DR EMBL; M24102; AAA30768.1; -.
DR PIR; A43646; XMB0.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_unccoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multigene family; Methylation.
KM INIT MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AE848 CRC64;

Query Match 93.6%; Score 1453.5; DB 1; Length 297;
Best Local Similarity 94.6%; Pred. No. 6.8e-123;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 3 DHANSLKDFLAGA VAAAVSKTAVAPIERVLLIQVHASKQISAEKQYKGIIDCVVRIP 62
DB 2 DQALSLKDFLAGA VAAVAISKTAVAPIERVLLIQVHASKQISAEKQYKGIIDCVVRIP 61
QY 63 KEQGFSLRWKENTLVNIRPYTQALNAPFDKQYKQLFLGVDNRKQWRPYRAGMLASGGA 122
DB 62 KEQGFSLRWKENTLVNIRPYTQALNAPFDKQYKQLFLGVDNRKQWRPYRAGMLASGGA 121
QY 123 AGATSLCVVYPLDPAFTRLADVDR-PAOREFHGADPCIIKIFPSDGLRGLYOGFNVSVQ 181
DB 122 AGATSLCVVYPLDPAFTRLADVDRKGAHQREFTGLGNCITIKIFPSDGLRGLYOGFNVSVQ 181
QY 182 GIIITRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVALLSYPFDTVRBRMMQOS 241
DB 182 GIIITRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVALLSYPFDTVRBRMMQOS 241
QY 242 GRKQADIMYTGTVDCWKRIADBEAKAFPKAGMSNVLRKMGGAVALVLYDEIKKTV 297
DB 242 GRKQADIMYTGTVDCWKRIADBEAPKAFPKAGMSNVLRKMGGAVALVLYDEIKKTV 297

RESULT 5
ADT2_MOUSE STANDARD; PRT; 298 AA.
AC P51881; O61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP-ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
DE SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=97059403; PubMed=8903724;  
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;  
 RT "Rapid evolution of human pseudautosomal genes and their mouse  
 homologs";  
 RL Mamm. Genome 7:25-30(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RA Sheldon J.G.;  
 RL Theis (1995), University of Cambridge, U.K.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv;  
 RA Cochet P., Laplace C.;  
 RL Submitted (FEB-1993) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP REVISIONS.  
 RA Laplace C.;  
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20432087; PubMed=10974536;  
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;  
 RT "Expression and sequence analysis of the mouse adenine nucleotide  
 translocase 1 and 2 genes";  
 RL Gene 254:57-66(2000).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U27316; AAC52838.1; -;  
 DR EMBL; U10404; AA19009.1; -;  
 DR EMBL; X70847; CA50196.1; -;  
 DR EMBL; AF240003; AAF64471.1; -;  
 DR MGI; MGI:1353496; Slc25a5.  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR InterPro; IPR002030; Mlt\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mltc\_carri; 3-  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;  
 Query Match 90.7%; Score 1408.5; DB 1; Length 298;  
 Best Local Similarity 89.6%; Pred. No. 7.3e-119;

Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;  
 QY 1 MGDAMSTLDPLAGAVAAVSKTAVAPIREVKILLQVQASKQISAEKQKGIIDCVR 60  
 DB 1 MTDAVSPADPLAGVAAVSKTAVAPIREVKILLQVQASKQITADKQKGIIDCVR 60  
 QY 1PKQGFSPFRGNLVNIRPEPQALNFAKDKYKQLFLGGVNRHQPFMFPNGNLASG 120  
 DB 61 IPKQGVLSFRGNLVNIRPEPQALNFAKDKYKQLFLGGVNRHQPFMFPNGNLASG 120  
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGR-AGREPHGLDCLIKIFKSDGLNGLYQGFNV 179  
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGRAGAREPHGLDCLIKIFKSDGLNGLYQGFNV 180  
 QY 180 VQGIITRAAVFGYDPAKGLPDPKXVHIVSMIAQSVTAVAGLISPPDYRRRMM 239  
 DB 181 VQGIITRAAVFGYDPAKGLPDPKXVHIVSMIAQSVTAVAGLISPPDYRRRMM 240  
 QY 240 QSGRRGADIMVTVDCMRKIAKDEGAKAPFGKAMSVNLRMGAFVLYVDEIKY 296  
 DB 241 QSGRRGADIMVTVDCMRKIAKDEGAKAPFGKAMSVNLRMGAFVLYVDEIKY 297  
 RESULT 6  
 ADT2\_RAT  
 ID ADT2\_RAT STANDARD; PRT; 298 AA.  
 AC Q09073;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 DE (Adenine nucleotide translocator 2) (ANT 2).  
 GN SLc25A5 OR ANT2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=94002161; PubMed=8399300;  
 RA Shinozaki Y., Kamada M., Yamazaki N., Terada H.;  
 RT "Isolation and characterization of cDNA clones and a genomic clone  
 encoding rat mitochondrial adenine nucleotide translocator";  
 RL Biochem. Biophys. Acta 1152:192-196(1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND  
 SKELETAL MUSCLE.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; D12771; BAA02238.1; -;  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR InterPro; IPR002030; Mlt\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mltc\_carri; 3-  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family.

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FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EE35 CRC64;

Query Match
Best Local Similarity 89.6%; Score 1407.5; DB 1; Length 298;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTDAAVSFAKDFLAGAANAISKTAVAPIERVKLLQVQHASKOITADKQYGIIDCVR 60
QY 61 IPKEQGLSPFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDHRKQFMRYPAGNLASG 120
DB 61 IPKEQGLSPFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDKRTQFMRYPAGNLASG 120
QY 121 GAAGTSLCPVYPLDPFAPRRLAADVGR-AGREPHGLDCCIIRKSGDLRLYGGFVNS 179
DB 121 GAAGTSLCPVYPLDPFAPRRLAADVGRAGREPHGLDCCIIRKSGDLRLYGGFVNS 180
QY 180 VGGIITPAAVYRGVYDTAKGMLPDPKRVHIFPMNIAOSVTAAGILSYEPDTPVRRMM 239
DB 181 VGGIITPAAVYRGVYDTAKGMLPDPKRVHIFPMNIAOSVTAAGILSYEPDTPVRRMM 240
QY 240 QSGRRKADIMTGTVDCKWKIAXDKGAKAFKFGANSVLRMGGAFTLVLYDEIKKY 296
DB 241 QSGRRKADIMTGTVDCKWKIAXDKGAKAFKFGANSVLRMGGAFTLVLYDEIKKY 297

RESULT 7
ADT2_HUMAN STANDARD; PRT; 298 AA.
ID ADT2_HUMAN STANDARD; PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLIC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wuzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Situno A., Nagaraia R.,
RA Mazzarella R.A., Schlesinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.

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RA Becker M., Graves T., Ozereky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
-----
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CC or send an email to license@ebi.ac.uk).
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CC EMBL; M57424; AAA51737.1; -
CC EMBL; J02683; AAA35579.1; -
CC EMBL; L78810; AAB39266.1; -
CC EMBL; AC004000; AAB96347.1; -
CC EMBL; J03591; AAA36749.1; -
CC PIR; A29132; A29132.
CC Genew; HGNC:10991; SLIC25A5.
DR MIM; 300150; -
DR GO; GO:0005887; C:Integral to plasma membrane; TMS.
DR GO; GO:0015207; P:adenine transporter activity; TMS.
DR GO; GO:0006832; P:small molecule transport; TMS.
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mltoc_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KV Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KV Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 6 6 V->L (IN REF. 2).
FT CONFLICT 66 66 G->E (IN REF. 2).
FT CONFLICT 111 111 R->L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V->G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match
Best Local Similarity 89.9%; Score 1398.5; DB 1; Length 298;
Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTDAAVSFAKDFLAGAANAISKTAVAPIERVKLLQVQHASKOITADKQYGIIDCVR 60
QY 61 IPKEQGLSPFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDHRKQFMRYPAGNLASG 120
DB 61 IPKEQGLSPFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDKRTQFMRYPAGNLASG 120

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QY 121 GAAGATSLCFYVPLDPAFRTLAADVGR-AQREFHGLDCCIITIKFKSDGLNGLYOGFNV 179  
 DB 121 GAAGATSLCFYVPLDPAFRTLAADVGRKARERFGLDCLVTKYSKIGLYOGFNV 180  
 QY 180 VGGIIRAYFVGYDPAKMLPDPKRVHIFVSMVIAQSVTAVALGLSYPPDYRRMM 239  
 DB 181 VGGIIRAYFVGYDPAKMLPDPKRVHIFVSMVIAQSVTAVALGLSYPPDYRRMM 240  
 QY 240 QSGRKGADIMYTGVDGCRKTADEGAKAFKGMNSVLRGMGAFVLYVDELKTY 296  
 DB 241 QSGRKGADIMYTGVDGCRKTADEGAKAFKGMNSVLRGMGAFVLYVDELKTY 297  
 RESULT 8  
 ADT3\_HUMAN  
 ID ADT3\_HUMAN STANDARD; PRT; 298 AA.  
 AC P12236; Q96C49;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP, ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)  
 DE (Adenine nucleotide translocator 3) (ANT 3).  
 GN SLIC25A6 OR ANT3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89236396; PubMed=2541251;  
 RA Cozens A.L., Runswick M.J., Walker J.B.;  
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
 ADP/ATP translocase";  
 RL J. Mol. Biol. 206:261-280 (1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
 RA Margolin J.F.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Cervix, Eye, and Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP SEQUENCE OF 36-298 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88124845; PubMed=2829183;  
 RA Houldsworth J., Attardi G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 level in adult human liver";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL: J03592; AAA6750.1; -;  
 CC EMBL: AY007135; AAG01998.1; -;  
 CC EMBL: BC007295; AAH07295.1; -;  
 CC EMBL: BC007850; AAH07850.1; -;  
 CC EMBL: BC008737; AAH08737.1; -;  
 CC EMBL: BC008935; AAH08935.1; -;  
 CC EMBL: BC014775; AAH14775.1; -;  
 CC PIR: S03894; S03894.  
 CC GeneW: HGNC:10992; SLIC25A6.  
 CC MIM: 300151; -;  
 CC GO: GO:0005744; C:mitochondrial inner membrane translocase co. . .; TAS.  
 CC GO: GO:0005471; F:ATP/ADP antiporter activity; TAS.  
 CC GO: GO:0006854; P:ATP/ADP exchange; TAS.  
 CC InterPro: IPR002067; Mlt\_carrier.  
 CC InterPro: IPR002030; Mlt\_uncoupling.  
 CC InterPro: IPR001993; Mitoch\_carrier.  
 CC Pfam: PF00153; mltc\_carri; 3\_  
 CC PRINTS: PR00926; MITOCARRIER.  
 CC PROSITE: PRO0784; MTNCOUPLING.  
 CC PROSITE: PS00215; MITOCH\_CARRIER; 3.  
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 100 1.  
 FT REPEAT 101 208 2.  
 FT REPEAT 209 298 3.  
 FT CONFLICT 105 108 S -> F (IN REF. 3; AAH14775).  
 FT CONFLICT 242 242 KHTQ -> RHA (IN REF. 4).  
 SQ SEQUENCE 298 AA; 3286 MM; 18534EP0E49672F CRC64;  
 Query Match 89.2%; Score 1385.5; DB 1; Length 298;  
 Best local similarity 87.2%; Pred. No. 8.4e-117;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGHANSLFLDPAFRTLAADVGRKARERFGLDCLVTKYSKIGLYOGFNV 60  
 DB 1 MGHANSLFLDPAFRTLAADVGRKARERFGLDCLVTKYSKIGLYOGFNV 60  
 QY 1 MTEPAISFADPFLAGGIAAISKTAVALPIRVKLLQVHASKIADKKYGLVDCIVR 60  
 DB 1 MTEPAISFADPFLAGGIAAISKTAVALPIRVKLLQVHASKIADKKYGLVDCIVR 60  
 QY 1 PKKQGLSFWRGNLANVIRFPTQANPAFKDKYKQLFLGVDVRHQRFRYFPAANTASG 120  
 DB 1 PKKQGLSFWRGNLANVIRFPTQANPAFKDKYKQLFLGVDVRHQRFRYFPAANTASG 120  
 QY 1 PKKQGLSFWRGNLANVIRFPTQANPAFKDKYKQLFLGVDVRHQRFRYFPAANTASG 120  
 DB 1 PKKQGLSFWRGNLANVIRFPTQANPAFKDKYKQLFLGVDVRHQRFRYFPAANTASG 120  
 QY 121 GAAGATSLCFYVPLDPAFRTLAADVGR-AQREFHGLDCCIITIKFKSDGLNGLYOGFNV 179  
 DB 121 GAAGATSLCFYVPLDPAFRTLAADVGRKARERFGLDCLVTKYSKIGLYOGFNV 180  
 QY 180 VGGIIRAYFVGYDPAKMLPDPKRVHIFVSMVIAQSVTAVALGLSYPPDYRRMM 239  
 DB 180 VGGIIRAYFVGYDPAKMLPDPKRVHIFVSMVIAQSVTAVALGLSYPPDYRRMM 240  
 QY 240 QSGRKGADIMYTGVDGCRKTADEGAKAFKGMNSVLRGMGAFVLYVDELKTY 296  
 DB 240 QSGRKGADIMYTGVDGCRKTADEGAKAFKGMNSVLRGMGAFVLYVDELKTY 297

ID	ADP3 BOVIN	STANDARD;	PRT;	298 AA.
AC	P32007			
DT	01-JUL-1993	(Rel. 26, Created)		
DT	01-JUL-1993	(Rel. 26, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	ADP, ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).			
CN	SLC25A6 OR ANT3.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxId=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89229093; PubMed=2540808;			
RA	Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;			
RT	"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";			
RU	Biochemistry 28:866-873(1989)			
CC	- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE			
CC	MITOCHONDRIAL INNER MEMBRANE.			
CC	- SUBUNIT: Homodimer.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial			
CC	inner membrane.			
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.			
CC	-----			
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CC	entities requires a license agreement (See <a href="http://www.isb-sdb.ch/announce/">http://www.isb-sdb.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sdb.ch">license@isb-sdb.ch</a> ).			
CC	-----			
DR	EMBL; M24103; AAA0769.1; -.			
DR	PIR; B43646; B43646.			
DR	InterPro; IPR002067; Mlt_carrier.			
DR	InterPro; IPR002030; Mlt_uncoupling.			
DR	InterPro; IPR001993; Mitoch_carrier.			
DR	Pfam; PF00153; mltc_carri_3.			
DR	PRINTS; PR00926; MITOCARRIER.			
DR	PRINTS; PR00784; MTUNCOUPLING.			
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.			
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;			
FT	Multigene family.			
FT	TRANSMEM 12 29 1 (POTENTIAL).			
FT	TRANSMEM 73 91 2 (POTENTIAL).			
FT	TRANSMEM 117 134 3 (POTENTIAL).			
FT	TRANSMEM 176 195 4 (POTENTIAL).			
FT	TRANSMEM 214 231 5 (POTENTIAL).			
FT	TRANSMEM 273 291 6 (POTENTIAL).			
FT	REPEAT 2 111 1.			
FT	REPEAT 112 111 2.			
FT	REPEAT 208 208 2.			
FT	REPEAT 209 298 3.			
SQ	SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;			
Query Match	88.9%; Score 1380.5; DB 1; Length 298;			
Best Local Similarity	86.9%; Pred. No. 2.4e-116;			
Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1				
QY	1 MGDHMSFLKDFLAGAANAASKTAVPIERVCLLLVOVHASKOISAEKQYKGIIDCVR	60		
DB	1 MTBQKISPAKOFIAGIAAISTKTAIVPIERVKLLLOVHASKOIAADKQYGIYDCIVR	60		
QY	61 IPKGGFLSPFRGNLANVIRYPTQALNFAFDKTKQLFLGGVDHKKQFWRFAQNLASG	120		
DB	61 IPKGGVLSFPRGNLANVIRYPTQALNFAFDKTKQLFLGGVDKRTQFWRFAQNLASG	120		

QY	121	GAAGTSCTCFYPYLPDPATRLAADVGR - AOGEEFGLGCCI.IKIFGSDGLRGLOGFENS 179
DB	121	GAAAGTSCTCFYPYLPDPATRLAADVGRSGSEHREFGLDCLVKITGSDGIRGLYOGFENS 180
QY	180	VOGIIITRYAAFYGVYDTAKGM.PDEKXNVI.FVSWMIAGSVTA VAGLLSYPPDTRRRMM 239
DB	181	VOGIIITRYAAFYGVYDTAKGM.PDEKXNTH.IVSWMIAGSVTA VAGVSYPPDTRRRMM 240
QY	240	QSGRGADIMTGTCTDCKRKLAKDGGATAFFYGANSNTLRGCGAFV.VLYOIEKKYV 297
DB	241	QSGRGADIMTGTCTDCKRKLAKDGGATAFFYGANSNTLRGCGAFV.VLYOIEKKYV 298
RESULT 10		
ADT_DROP	ADT_DROP	STANDARD; PRT; 299 AA.
ID	Q26365; P91614; Q26554; Q95S30; Q9VZ70;	
AC	15-JUL-1998 (Rel. 36, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	15-SEP-2003 (Rel. 42, Last annotation update)	
DE	ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT) (Stress sensitive B protein).	
GN	SESB OR A/A-T OR CGA16944.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=92389367; PubMed=1387687;	
RA	Louvi A., Tsitilon S.G.;	
RT	"A cDNA clone encoding the ADP/ATP translocase of Drosophila melanogaster shows a high degree of similarity with the mammalian ADP/ATP translocases";	
RL	J. Mol. Evol. 35:44-50(1992).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=94350065; PubMed=7520869;	
RA	Hutter P., Karch F.;	
RT	"Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila.";	
RL	Experientia 50:749-762(1994).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Oregon-R;	
RL	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;	
RN	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.	
RP	[4]	
RC	SEQUENCE FROM N.A.	
RX	MEDLINE=20196006; PubMed=10731132.	
RA	Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	
RA	George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,	
RA	wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Milos G.L.G.,	
RA	Abail J.F., Agbani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,	
RA	Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bhotishav S.,	
RA	Borkova D., Botchan M.R., Bouck J., Brockstein P., Brodtier P.,	
RA	Burtis K.C., Buesam D.A., Butler H., Cadieu B., Center A., Chandra I.,	
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Dey S.A., Dew I., Dietz S.M.,	
RA	Dodson K.C., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	
RA	Glaser C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,	
RA	Gloder A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	
RA	Hoselin D., Houston K.A., Howland T.U., Wei M.-H., Ibegwam C.,	
RA	Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lesko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusseren D.R., Pacle J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Stykars R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Berkeley; TISSUE-larva, Ovary, and Pupae;  
 RX MEDLINE=22426066; PubMed=12537569;  
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champagne M.,  
 RA George R.A., Guarin H., Krommiller B., Pacle J.M., Park S., Wan K.H.,  
 RA Rubin G.M., Celinker S.E.;  
 RT "A Drosophila full-length cDNA resource.";  
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).  
 CC -1- FUNCTION: Catalyzes the exchange of ADP and ATP across the  
 CC mitochondrial inner membrane.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- DOMAIN: Composed of three homologous domains.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

Query Match 79.9%; Score 1241; DB 1; Length 299;  
 Best Local Similarity 79.7%; Pred. No. 7, 3e-104;  
 Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;  
 QY 5 AMSFLADPLAGAAVAASKTAVAPIERVKLLQVHASKOISAKQYKGIIDCVRIKPE 64  
 DB 7 AVGVKDPFAAGSISAAVSTKAVAPIERVKLLQVHISKOISPDQYKQGWDCFRIPKE 66  
 QY 65 QGFLSFVRGMLAVIRFPFQALNFAKDKYKQLFLGVDRHQFMYFPAGNLASGGAAG 124  
 DB 67 QGSSFFVRGMLAVIRFPFQALNFAKDKYKQVFLGVDRHQFMYFPAGNLASGGAAG 126  
 QY 125 ATSLCFYPLDPFARTRLAADVGRRAOREFGLGDCIIXFKPSDGLRGLYOGFNVSGIIT 184  
 DB 127 ATSLCFYPLDPFARTRLAADVGRRAOREFGLGDCIIXFKPSDGLRGLYOGFNVSGIIT 186  
 QY 185 IYRAAYFGVDTARAGMLPDPKNTPIYISMAIAQVVTVAIVSYPFDTVRBRMMQSGRK 244  
 DB 187 IYRAAYFGVDTARAGMLPDPKNTPIYISMAIAQVVTVAIVSYPFDTVRBRMMQSGRK 246  
 QY 245 GADIMYGTGDCMRKIAKDGAKAFKFGANSNLRGCGAPVLYNREIK 295  
 DB 247 ATEVYNTLHCWATIAKQEGTGAFFKGFARSNILRTGAFVLYNREIK 297  
 RESULT 11  
 ADT\_ANOGA STANDARD; PRT; 301 AA.  
 ID ADT\_ANOGA  
 AC Q27238;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
 DE translocator) (ANT).  
 OS Anopheles gambiae (African malaria mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.  
 OX NCBI\_TaxID=7165;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=G3;  
 RX MEDLINE=94348635; PubMed=8069414;  
 RA Beard C.B., Crews-Oyen A.B., Kumar V.K., Collins F.H.;  
 RT "A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles  
 RL gambiae.";  
 RL Insect Mol. Biol. 3:35-40(1994).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

FT TRANSMEM 178 197 4 (POTENTIAL).  
 FT TRANSMEM 216 233 5 (POTENTIAL).  
 FT TRANSMEM 275 293 6 (POTENTIAL).  
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;  
 Query Match 74.9%; Score 1162.5; DB 1; Length 301;  
 Best Local Similarity 76.3%; Pred. No. 7,9e-97;  
 Matches 223; Conservative 26; Mismatches 40; Indels 1; Gaps 1;  
 QY 6 WSFLKDFLAGAANAASVSTAVAPIERVKLLQVQASAKQISAKQYKIIDCVARIPREQ 65  
 Db 8 YGFAPKDFLAGGISAASVSTAVAPIERVKLLQVQASAKQIADVCKYKIIDCVARIPREQ 67  
 QY 66 GFLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDHKKQFRRYFAGNLASGGAAGA 125  
 Db 68 GIGAFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDHKKQFRRYFAGNLASGGAAGA 127  
 QY 126 TSLCFVYPLDPAFTRTLADVGRRRA-QREFHGIDCIIIFKSDGLRGLYOGFNVSVOGII 184  
 Db 128 TSLCFVYPLDPAFTRTLADVGRRRA-QREFHGIDCIIIFKSDGLRGLYOGFNVSVOGII 187  
 QY 185 IYRAAYFGVYDTAKGMLPDPKXVNIIFVSMWIAQSVTAVALGSLYFPDTRRRMMQSGRK 244  
 Db 188 IYRAAYFGVYDTAKGMLPDPKXVNIIFVSMWIAQSVTAVALGSLYFPDTRRRMMQSGRK 247  
 QY 245 GADIMYTGTVDCMRKIADEGAKAFPKGAMSNVLRGAGAFVLYLDEIKY 294  
 Db 248 KSEVWYKNTLDQWVXIGKQEGSGAFPKGAFSVNLRTGALVLYLDEIKY 297  
 RESULT 12  
 ADT\_CHLRE STANDARD; PRT; 339 AA.  
 ID ADT\_CHLRE STANDARD; PRT; 339 AA.  
 AC P31692;  
 DT 01-JUN-1993 (Rel. 26, Last sequence update)  
 DT 01-JUN-1993 (Rel. 26, Last sequence update)  
 DT 15-OCT-1998 (Rel. 36, Last annotation update)  
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).  
 OS Chlorella kesselii.  
 CC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.  
 CC NCBI\_TaxID=3074;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92084708; PubMed=1748677;  
 RA Hilgarch C., Sauer N., Tanner W.;  
 RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";  
 RL J. Biol. Chem. 266:24044-24047(1991).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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 CC EMBL; M76669; AAA33027.1; -.  
 DR PIR; A41677; A41677.  
 DR InterPro; IPR002067; Mlt carrier.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR Pfam; PF00153; mito\_carr; 3\_  
 DR PRINTS; PR000926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.

KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 45 62 1 (POTENTIAL).  
 FT TRANSMEM 108 126 2 (POTENTIAL).  
 FT TRANSMEM 151 168 3 (POTENTIAL).  
 FT TRANSMEM 209 228 4 (POTENTIAL).  
 FT TRANSMEM 248 265 5 (POTENTIAL).  
 FT TRANSMEM 304 322 6 (POTENTIAL).  
 SQ SEQUENCE 339 AA; 36686 MW; 54479734A3B3942 CRC64;  
 Query Match 62.7%; Score 973.5; DB 1; Length 339;  
 Best Local Similarity 65.3%; Pred. No. 7,6e-80;  
 Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;  
 QY 7 SFLKDFLAGAANAASVSTAVAPIERVKLLQVQASAKQISAKQYKIIDCVARIPREQ 64  
 Db 40 AFVLDLLAGAGAGAIISKTAAPAPIERVKLLQVQASAKQISAKQYKIIDCVARIPREQ 99  
 QY 65 GFLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDHKKQFRRYFAGNLASGGAAGA 124  
 Db 100 QGVASFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDHKKQFRRYFAGNLASGGAAGA 158  
 QY 125 ATSLCFVYPLDPAFTRTLADVGRRRA-QREFHGIDCIIIFKSDGLRGLYOGFNVSVOGII 184  
 Db 159 AGSLIIVYPLDPAFTRTLADVGRRRA-QREFHGIDCIIIFKSDGLRGLYOGFNVSVOGII 218  
 QY 185 IYRAAYFGVYDTAKGMLPDPKXVNIIFVSMWIAQSVTAVALGSLYFPDTRRRMMQSGRK 243  
 Db 219 IYRAAYFGVYDTAKGMLPDPKXVNIIFVSMWIAQSVTAVALGSLYFPDTRRRMMQSGRK 276  
 QY 244 KADIMYTGTVDCMRKIADEGAKAFPKGAMSNVLRGAGAFVLYLDEIKY 297  
 Db 277 GGERQYNGTIDCMRKIADEGAKAFPKGAMSNVLRGAGAFVLYLDEIKY 329  
 RESULT 13  
 ADT\_CHLRE STANDARD; PRT; 308 AA.  
 ID ADT\_CHLRE STANDARD; PRT; 308 AA.  
 AC P27080;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).  
 OS Chlamydomonas reinhardtii.  
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonas.  
 CC NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=FUD4-R2;  
 RX MEDLINE=93204887; PubMed=8455552;  
 RA Sharpe J.A., Day A.;  
 RT "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.";  
 RL Mol. Gen. Genet. 237:134-144(1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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 CC EMBL; X65194; CAA46311.1; -.  
 DR

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DR PIR, S30259; S30259.
DR InterPro; IPR002067; Mit carrier.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 217 234 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
SQ SEQUENCE 308 AA; 33528 MW; D47CF0E72B7A53F CRC64;

Query Match 49.6%; Score 770.5; DB 1; Length 308;
Best Local Similarity 52.6%; Pred. No. 1e-61;
Matches 159; Conservative 49; Mismatches 77; Indels 17; Gaps 6;

QY 7 SFLDPLAGVAANAASKTAVAPIRVYKLLQVQ-HASQISAERQYGIIDCVIRIRKQ 65
DB 7 NFMVDFLAGGSAASVSKTAAPLIEVKLLIONDEMTKGRSLASPYKIGECFVRYVER 66
QY 66 GFLSFMRGNLANVIRYPTQALNFAFKDYKQLFGVDVDRHKQFWRYPAGNLAGGAAGA 125
DB 67 GFLSLMGNLANVIRYPTQALNFAFKDYKQLFGVDVDRHKQFWRYPAGNLAGGAAGA 124
QY 126 TSLCFVPLDFAFRLADVGR---AOREFHGIDCIIFKSDGLRGLYQGFNVSVQ 181
DB 125 VLSLFVYSLDYARFRLANDAKSAGKGGDQFNGLVYRRTIASDGIAGLYRGFNISCV 184
QY 182 GIITRYAAYRGVYDTAG-MLPDPKNVHIFVSMIAQSVTAAGLSTPPTVRRMMQ 240
DB 185 GIIVYRGLYFGMYSLKPVVLVGPANNFLAFLGWMGITTGAGLASYPIDITIRRMNT 244
QY 241 SGRKADIMYGTVDQWRKIAKDEGAKAFKAGANSVLRGMAFVLVYDEI-----K 294
DB 245 S---GSANVYSFHCQGEIVKNEGMSLFRGAGANILIRAVAGVLAGYDQLQVILLGK 301
QY 295 KY 296
DB 302 KY 303

RESULT 14
ADT1 MAIZE STANDARD; PRT; 387 AA.
ID ADT1 MAIZE STANDARD; PRT; 387 AA.
AC P04709;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN ANTI OR ANT-GI.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOTIND-FR7205034;
RA MEDLINE=91322533; PubMed=1863785;
RA Winking B.M., Day C.D., Sarah C.J., Leaver C.J.;
RT "Nucleotide sequence of two cDNAs encoding the adenine nucleotide translocator from Zea mays L."
RL Plant Mol. Biol. 17:305-307(1991).
RN [2]
RP SEQUENCE OF 59-387 FROM N.A.
RC STRAIN=CV, B37N;
RA MEDLINE=89338399; PubMed=2547608;
RA Leaver C.J., Bathgate B., Baker A.;
RT "Two genes encode the adenine nucleotide translocator of maize

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RT mitochondria. Isolation, characterisation and expression of the
RT structural genes."
RL Eur. J. Biochem. 183:303-310(1989).
RN [3]
RP SEQUENCE OF 70-387 FROM N.A.
RX MEDLINE=85297781; PubMed=2994015;
RA Baker A., Leaver C.J.;
RT "Isolation and sequence analysis of a cDNA encoding the ATP/ADP translocator of Zea mays L."
RL Nucleic Acids Res. 13:5857-5867(1985).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC -----
DR EMBL; X57556; CA40781.1; -
DR EMBL; X15711; CA33742.1; -
DR EMBL; X02842; CA26600.1; -
DR PIR; S14876; S14876.
DR MaizeDB; 17145; -
DR InterPro; IPR002067; Mit carrier.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Transic peptide; Multigene family.
FT TRANSLIT 77 MITOCHONDRION.
FT CHAIN 78 387 ADP,ATP CARRIER PROTEIN 1.
FT TRANSMEM 91 108 1 (POTENTIAL).
FT TRANSMEM 153 171 2 (POTENTIAL).
FT TRANSMEM 196 213 3 (POTENTIAL).
FT TRANSMEM 257 276 4 (POTENTIAL).
FT TRANSMEM 296 313 5 (POTENTIAL).
FT TRANSMEM 352 370 6 (POTENTIAL).
FT CONFLICT 102 K -> E (IN REF. 2).
FT CONFLICT 154 N -> Y (IN REF. 3).
SQ SEQUENCE 387 AA; 42391 MW; DE73BB0F478BD57D CRC64;

Query Match 48.7%; Score 756.5; DB 1; Length 387;
Best Local Similarity 53.8%; Pred. No. 2.4e-60;
Matches 164; Conservative 41; Mismatches 77; Indels 23; Gaps 7;

QY 7 SFLDPLAGVAANAASKTAVAPIRVYKLLQVQ-HASQISAERQYGIIDCVIRIRKQ 65
DB 7 NFMVDFLAGGSAASVSKTAAPLIEVKLLIONDEMTKGRSLASPYKIGECFVRYKDE 145
QY 66 GFLSFMRGNLANVIRYPTQALNFAFKDYKQLFGVDVDRHKQFWRYPAGNLAGGAAGA 125
DB 146 GFLSLMGNLANVIRYPTQALNFAFKDYKQLFGVDVDRHKQFWRYPAGNLAGGAAGA 124
QY 126 TSLCFVPLDFAFRLADVGR---AOREFHGIDCIIFKSDGLRGLYQGFNVSVQ 182
DB 205 SLSLFVYSLDYARFRLANDAKSAGKGGDQFNGLVYRRTIKSDGIAGLYRGFNISCV 264
QY 183 IITRYAAYRGVYDTAK-----GMLPDPKNVHIFVSMIAQSVTAAGLSTPPTVRRM 237
DB 265 IIVYRGLYFGLYSIRKVVLTGNLQD---NFPASFLGWLITGAGLASYPIDTVRRM 320
QY 238 MMSGKRGADIMYGTVDQWRKIAKDEGAKAFKAGANSVLRGMAFVLVYDEI----- 293
DB 321 MMSGGA---VKYSSIDARQQLIKKGPKSLFRGAGANILIRAVAGVLAGYDQLQILF 377

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Qy 294 --KXY 296  
Db 378 FGKXY 382

RESULT 15  
ADT\_SCHPO STANDARD; PRT; 322 AA.  
AC Q09188; 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE ADP, ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).  
GN ANCL OR SPBC530.10C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;  
OC NCBI TaxID=4896;  
CX [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=972;  
RC MEDLINE=96257204; PubMed=8675018;  
RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;  
RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae."  
RT Gene 171:113-117(1996).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=972;  
RC MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holtrope S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean C., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Wheller-Auer S., Gabel C., Fuchs M., Pritze C., Holzer E., Moestl D., Hilbert H., Botzys K., Langer I., Beck A., Leinrich H., Reinhardt K., Pohl T.M., Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Sipakovski G.V., Ussery D., Barrett B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe."  
RL Nature 415:871-880(2002).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

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CC  
CC EMBL; 249974; CA90275.1; -  
DR EMBL; AL023634; CA19176.1; -  
DR PIR; T40526; T40526.  
DR GenBank; SPBC530.10C; -  
DR InterPro; IPR002067; Mito\_carrier.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mto\_carr; 3.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 2.  
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
FT TRANSMEM 28 48 1 (POTENTIAL).  
FT TRANSMEM 93 111 2 (POTENTIAL).  
FT TRANSMEM 131 151 3 (POTENTIAL).  
FT TRANSMEM 197 217 4 (POTENTIAL).  
FT TRANSMEM 222 242 5 (POTENTIAL).  
FT TRANSMEM 289 309 6 (POTENTIAL).  
SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;  
Query Match 48.5%; Score 752.5; DB 1; Length 322;  
Best Local Similarity 52.9%; Pred. No. 4,4e-60;  
Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;  
Qy 7 SFLKDLPLAGVAANAASVTAVAPIRRVKLLQVQASKOISAEK--QYKGIIDCVVRIPK 63  
Db 26 TFFPDPFMVGGVSAASVSTAAPIRIVKLLIQNQ--DEMIRAGRISHRYKIGSECFKRTVA 83  
Qy 64 HQGFLSPFRGNLANVIRYPPPTQALNPAFKDKYKQLPFGVDRHROFWRVYFAGNLASGAA 123  
Db 84 BEGVISLMRGNTAVLVYFPQALNPAFKDKYKQMF-GYKKERGVYAKWFGNLASGAA 142  
Qy 124 GATSLCEVYPLDFAETRLAAD--VGRRAQREPHGLDCIIRKPSDGLRGLYOGFNVSV 180  
Db 143 GAASLLFVYSLDARTLTLANDAKSAKKGERQFGLVDVVRKTRSDGLRGLYGFSPSV 202  
Qy 181 QGIIYPAAYFQVYDIAKG-MLPDPKQVHIFVSMIAOSTAVAVGLISPPDYTRRRMM 239  
Db 203 VGIIVYRGLYFGMDILKPVVLVGLPGLNPLASFLGLMAVVTGSGVASYPLDITRRMM 262  
Qy 240 QSGRKGADIVTGVDCMRKIANDEGAKAPFKGMSNVNLGMSGAFVLVYDEIK 294  
Db 263 TSGEA--VKYSSFEGRQILAKESARSPFKGANILKGVAGVLSITDQV 314

Search completed: December 18, 2003, 12:41:23  
Job time : 9.31467 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:01 / Search time 30.598 Seconds

(without alignments)  
2504.793 Million cell updates/sec

Title: US-09-811-131-31

Perfect score: 1553  
Sequence: 1 MGDHANSFLDPLAGAVAA.....LRGNGAFVLYDEIKKYV 297

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1464.5	94.3	298	6	O46373
2	1462.5	94.2	298	11	O8BVI9
3	1411.5	90.9	298	6	O8SOH5
4	1392.5	89.7	298	13	O8AYM3
5	1377.5	88.7	298	13	O9YIC4
6	1377.5	88.7	298	13	O9YIC4
7	1375.5	88.6	298	13	O9YIC4
8	1374.5	88.5	298	13	O9YIC4
9	1366.5	88.0	298	13	O9YIC4
10	1245.5	80.2	299	5	O9SVX4
11	1241.5	79.9	300	5	O9SVX4
12	1241.5	79.9	312	5	O8IRAO
13	1234.5	79.5	317	13	O91336
14	1183	76.2	288	5	O44094
15	1183	76.2	288	5	O44093
16	1180.5	76.0	254	11	O8BKQ5

17	1147	73.9	307	5	O62526	O62526 drosophila
18	1139.5	73.4	304	5	O25129	O25129 halocynthia
19	1101.5	70.9	315	4	O9HOC2	O9HOC2 homo sapien
20	1045.5	67.3	313	5	P91410	P91410 caenorhabdi
21	1043.5	67.2	313	5	O21103	O21103 caenorhabdi
22	1042	67.1	310	10	O8H727	O8H727 phytophthor
23	1037.5	66.8	300	5	O45865	O45865 caenorhabdi
24	1005.5	64.7	300	5	O01813	O01813 caenorhabdi
25	993.5	64.0	300	5	O17407	O17407 caenorhabdi
26	989.5	63.7	309	5	O97470	O97470 dictyosteli
27	959	61.8	307	8	O9XM22	O9XM22 ascaris suu
28	950	61.2	318	5	O9BJ36	O9BJ36 toxoplasma
29	926.5	59.7	301	5	O8MVR4	O8MVR4 euploties sp
30	916.5	59.0	308	5	O8MVR8	O8MVR8 nycottherus
31	914.5	58.9	305	5	O8MVR7	O8MVR7 nycottherus
32	913.5	58.8	306	5	O8MVR5	O8MVR5 nycottherus
33	908.5	58.5	301	5	O81J34	O81J34 plasmodium
34	906.5	58.4	308	5	O8MVR6	O8MVR6 nycottherus
35	905.5	58.3	301	5	O25692	O25692 plasmodium
36	904.5	58.2	301	5	O26006	O26006 plasmodium
37	841.5	54.2	170	6	O9X869	O9X869 sus scrofa
38	772	49.7	306	5	O18683	O18683 caenorhabdi
39	757.5	48.8	305	3	O9P8M1	O9P8M1 yarrowia 1i
40	750.5	48.3	307	5	O76286	O76286 trypanosoma
41	748.5	48.2	303	3	O74260	O74260 candida par
42	746.5	48.1	379	10	O49447	O49447 arabidopsis
43	745.5	48.0	326	5	P91270	P91270 caenorhabdi
44	743.5	47.9	307	5	O26697	O26697 trypanosoma
45	743	47.8	302	3	O8J0M2	O8J0M2 yarrowia 1i

## ALIGNMENTS

### RESULT 1

O46373 PRELIMINARY; PRT; 298 AA.

AC O46373; (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)

DE ADP/ATP translocase.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

FN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RA Yamaguchi N., Kasai M.;

RT "Identification of a 30kDa calsequestrin-binding protein, which regulates calcium release from sarcoplasmic reticulum of rabbit skeletal muscle."

RT J. Biochem. 335:541-547 (1998).

RL -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

CC EMBL; AB009386; BA23777.1; -

DR InterPro; IPR001993; Mitoch\_carrier.

DR InterPro; IPR002067; Mit\_carrier.

DR InterPro; IPR002030; Mit\_uncoupling.

DR Pfam; PF00153; mito\_carr1.3.

DR PRINTS; PR00926; MITOCARRIER.

DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH\_CARRIER; 3.

KW Membrane; Transmembrane; Transport.

SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 94.3%; Score 1464.5; DB 6; Length 298;  
Best Local Similarity 94.6%; Pred. No. 7.2e-129;  
Matches 282; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

OY 1 MGDHANSFLDPLAGAVAAVKTAAPVIERVLLLOVCHASKQISAEKQYKIIIDCVR 60  
DB 1 MSDHANSFLDPLAGAVAAVSKTAAPVIERVLLLOVCHASKQISAEKQYKIIIDCVR 60



```

QY 61 IPKGGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGQVDRHKOFRMYFAGNLASG 120
DB 61 IPKGGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGQVDRHKOFRMYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDGDCIIRKPSGLGLYOGFNV 179
DB 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDGDCIIRKPSGLGLYOGFNV 180
QY 180 VGGIITVAAAYFGVDTAKGMLPDPKXVHIFVSMWIAOSVTAVALGSLSPEDTVARRMM 239
DB 181 VGGIITVAAAYFGVDTAKGMLPDPKXVHIFVSMWIAQVTAVALGSLSPEDTVARRMM 240
QY 240 QSGRGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRMGCAFVLVYDEIKKY 297
DB 241 QSGRGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRMGCAFVLVYDEIKKY 298

```

## RESULT 2

```

Q8BV19 PRELIMINARY; PRT; 298 AA.
ID 08BV19
AC 08BV19;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN (1)
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA THE FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK078077; BAC37117.1;
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

```

Query Match 94.2%; Score 1462.5; DB 11; Length 298;  
 Best Local Similarity 94.0%; Pred. No. 1.1e-128;  
 Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

```

QY 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHSKQISAEKQYKGIIDCVYR 60
DB 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHSKQISAEKQYKGIIDCVYR 60
QY 61 IPKGGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGQVDRHKOFRMYFAGNLASG 120
DB 61 IPKGGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGQVDRHKOFRMYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDGDCIIRKPSGLGLYOGFNV 179
DB 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDGDCIIRKPSGLGLYOGFNV 180
QY 180 VGGIITVAAAYFGVDTAKGMLPDPKXVHIFVSMWIAOSVTAVALGSLSPEDTVARRMM 239
DB 181 VGGIITVAAAYFGVDTAKGMLPDPKXVHIFVSMWIAQVTAVALGSLSPEDTVARRMM 240
QY 240 QSGRGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRMGCAFVLVYDEIKKY 297
DB 241 QSGRGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRMGCAFVLVYDEIKKY 298

```

## RESULT 3

```

Q8SOH5 PRELIMINARY; PRT; 298 AA.
ID 08SOH5
AC 08SOH5;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

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DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN (1)
RC SEQUENCE FROM N.A.
RP Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RT differences in its isoforms."
RL Mitochondrion 1:371-379 (2002).
DR EMBL; AB065433; BAB84673.1;
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32955 MW; CB6897B987B79C0 CRC64;

```

Query Match 90.9%; Score 1411.5; DB 6; Length 298;  
 Best Local Similarity 89.9%; Pred. No. 6.6e-124;  
 Matches 267; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

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QY 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHSKQISAEKQYKGIIDCVYR 60
DB 1 MTDAVSPADKDFLAGAANAASKTAVAPIERVKLLQVQHSKQITADKQYKGIIDCVYR 60
QY 61 IPKGGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGQVDRHKOFRMYFAGNLASG 120
DB 61 IPKGGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGQVDRHKOFRMYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDGDCIIRKPSGLGLYOGFNV 179
DB 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDGDCIIRKPSGLGLYOGFNV 180
QY 180 VGGIITVAAAYFGVDTAKGMLPDPKXVHIFVSMWIAOSVTAVALGSLSPEDTVARRMM 239
DB 181 VGGIITVAAAYFGVDTAKGMLPDPKXVHIFVSMWIAQVTAVALGSLSPEDTVARRMM 240
QY 240 QSGRGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRMGCAFVLVYDEIKKY 296
DB 241 QSGRGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRMGCAFVLVYDEIKKY 297

```

## RESULT 4

```

Q8AVM3 PRELIMINARY; PRT; 298 AA.
ID 08AVM3
AC 08AVM3;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE ATP/ADP antiporter.
GN AVANT.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9931;
RN (1)
RC SEQUENCE FROM N.A.
RP Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
RT and ANT mRNA in chicken skeletal muscle."
RL FEBS Lett. 0:0-0 (2002).
DR EMBL; AB088686; BAC15533.1;
SQ SEQUENCE 298 AA; 32847 MW; 1174C5E6400A10D CRC64;

```

Query Match 89.7%; Score 1392.5; DB 13; Length 298;  
 Best Local Similarity 88.3%; Pred. No. 4e-122;  
 Matches 263; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

```

QY 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHSKQISAEKQYKGIIDCVYR 60

```



```

Db      1 MADQALISFLKDFLAGVAAAIKSTAVAPIERVKLLIQVHASKQITADKQYKGIIDCVR 60
Qy      61 IPKQGFSLFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDNRHQFMRYPFAGNLASG 120
Db      61 IPKQGFVSLFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDNRHQFMRYPFAGNLASG 120
Qy      121 GAAGATSLCFVYPLDPFARTLADVGR-AOREFHGLGDCIITIKIFKSGDLRGLYOGFNVS 179
Db      121 GAAGATSLCFVYPLDPFARTLADVGR-AOREFHGLGDCIITIKIFKSGDLRGLYOGFNVS 180
Qy      180 VQGIITIRAAVFGYITDAKGMLPDPKXVHIFVSMIAQSTYAVAGLSYPPDYRRRMM 239
Db      181 VQGIITIRAAVFGYITDAKGMLPDPKXVHIFVSMIAQSTYAVAGLSYPPDYRRRMM 240
Qy      240 QSGRKGADIMYTGITDCMRKTIADGEGAKAFPGKAMSVNLKMGAFVLVLYDEIKKYV 297
Db      241 QSGRKGADIMYTGITDCMRKTIADGEGAKAFPGKAMSVNLKMGAFVLVLYDEIKKYV 298

RESULT 5
Qy      09YIC4 PRELIMINARY; PRT; 298 AA.
ID      09YIC4
AC      09YIC4;
DT      01-MAY-1999 (TReMBLrel. 10, Created)
DT      01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      ADP/ATP translocase.
OS      Rana rugosa (Wrinkled frog).
OC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Buteleostomi;
OX      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
RN      NCB1_TaxID=8410;
RP      [1]
RX      MEDLINE=99083429; PubMed=9866197;
RA      Miura I., Ohnami H., Nakamura M., Ichikawa Y., Saitoh K.;
RT      "The origin and differentiation of the heteromorphic sex chromosomes
RT      Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT      a sex-linked gene, ADP/ATP translocase."
RL      Mol. Biol. Evol. 15:1612-1619(1998).
CC      -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL; AB008457; BAA36507.1;
DR      InterPro; IPR001993; Mitoch_carrier.
DR      InterPro; IPR002067; Mit_carrier.
DR      InterPro; IPR002030; Mit_uncoupling.
DR      Pfam; PF00153; mito_carri_3.
DR      PRINTS; PR00926; MITOCARRIER.
DR      PRINTS; PR00784; MTUNCOUPLING.
DR      PROSITE; PS00215; MITOCH_CARRIER; 3.
KM      Membrane; Transmembrane; Transport.
SQ      SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match      88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 1e-120;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

```

```

Db      241 QSGRKGADIMYTGITDCMRKTIADGEGAKAFPGKAMSVNLKMGAFVLVLYDEIKKYV 298
Qy      241 QSGRKGADIMYTGITDCMRKTIADGEGAKAFPGKAMSVNLKMGAFVLVLYDEIKKYV 297

RESULT 6
Qy      09PRH1 PRELIMINARY; PRT; 298 AA.
ID      09PRH1
AC      09PRH1;
DT      01-MAY-2000 (TReMBLrel. 13, Created)
DT      01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      ADP/ATP translocase.
OS      Rana rugosa (Wrinkled frog).
OC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Buteleostomi;
OX      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
RN      NCB1_TaxID=8410;
RP      [1]
RX      MEDLINE=99083429; PubMed=9866197;
RA      Miura I., Ohnami H., Nakamura M., Ichikawa Y., Saitoh K.;
RT      "The origin and differentiation of the heteromorphic sex chromosomes
RT      Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT      a sex-linked gene, ADP/ATP translocase."
RL      Mol. Biol. Evol. 15:1612-1619(1998).
CC      -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL; AB008453; BAA36513.1;
DR      EMBL; AB008456; BAA36506.1;
DR      EMBL; AB008461; BAA36511.1;
DR      EMBL; AB008462; BAA36512.1;
DR      InterPro; IPR001993; Mitoch_carrier.
DR      InterPro; IPR002067; Mit_carrier.
DR      InterPro; IPR002030; Mit_uncoupling.
DR      Pfam; PF00153; mito_carri_3.
DR      PRINTS; PR00926; MITOCARRIER.
DR      PRINTS; PR00784; MTUNCOUPLING.
DR      PROSITE; PS00215; MITOCH_CARRIER; 3.
KM      Membrane; Transmembrane; Transport.
SQ      SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match      88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 1e-120;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

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OS Brachydanio rerio (zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22035902; PubMed=12006978;  
 RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,  
 Bugnès S., Haldt M., Artzt K., Farrington S., Lin S.-Y., Nielsen R.M.,  
 Hopkins N.;  
 RT "Insertional mutagenesis in zebrafish rapidly identifies genes  
 essential for early vertebrate development.";  
 RL Nat. Genet. 31:135-140(2002).  
 DR EMBL; AF506216; AAM34660.1; -  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carri\_3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 SQ SEQUENCE 298 AA; 32763 MW; D7863CF65C51D39 CRC64;

Query Match 88.6%; Score 1375.5; DB 13; Length 298;  
 Best Local Similarity 86.9%; Pred. No. 1.6e-120;  
 Matches 257; Conservative 22; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHMSFLDPLAGAAVAASKTAVAPIERVKLLLOVQHSKQISAEKQYGIIDCVR 60  
 Db 1 MSETISPAKDFLAGAAVAASKTAVAPIERVKLLLOVQHSKQITADKQYGIIDCVR 60  
 Qy 61 IPKQGFSLFWRGMLAVIRFFPTQALNFAFKDKYKQLFLGVDRHKOFWRYFAGNLASG 120  
 Db 61 IPKQGFSLFWRGMLAVIRFFPTQALNFAFKDKYKQLFLGVDRHKOFWRYFAGNLASG 120  
 Qy 121 GAAGATSLCFYYPDPARTRLAADVGR-AQREPHGLDCCIIFKPSDGLKGLYQGFNV 179  
 Db 121 GAAGATSLCFYYPDPARTRLAADVGR-AQREPHGLDCCIIFKPSDGLKGLYQGFNV 179  
 Qy 121 GAAGATSLCFYYPDPARTRLAADVGR-AQREPHGLDCCIIFKPSDGLKGLYQGFNV 180  
 Db 121 GAAGATSLCFYYPDPARTRLAADVGR-AQREPHGLDCCIIFKPSDGLKGLYQGFNV 180  
 Qy 180 VGGIIIVRAAYFGYDTAKGMLPDPKXVHIFVSMIAQSTAVAGLLSYPPDTYRRMM 239  
 Db 180 VGGIIIVRAAYFGYDTAKGMLPDPKXVHIFVSMIAQSTAVAGLLSYPPDTYRRMM 239  
 Qy 181 VGGIIIVRAAYFGYDTAKGMLPDPKXVHIFVSMIAQSTAVAGLLSYPPDTYRRMM 240  
 Db 181 VGGIIIVRAAYFGYDTAKGMLPDPKXVHIFVSMIAQSTAVAGLLSYPPDTYRRMM 240  
 Qy 240 QSGRKGADIMTYGVDCWCKRIAKDEGAKAFKAGMSVNLKGAFVLVLYDEIKKYV 297  
 Db 241 QSGRKGADIMTYGVDCWCKRIAKDEGAKAFKAGMSVNLKGAFVLVLYDEIKKYV 298

## RESULT 8

Q9PRH2 PRELIMINARY; PRT; 298 AA.  
 AC Q9PRH2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS Rana rugosa (Wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 NCBI\_TaxID=8410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99083429; PubMed=9866197;  
 RA Miura T., Ohnishi H., Nakamura M., Ichikawa Y., Saitoh K.;  
 RT "The origin and differentiation of the heteromeric sex chromosomes  
 Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of  
 a sex-linked gene, ADP/ATP translocase.";  
 RL Mol. Biol. Evol. 15:1612-1619(1998).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AB008460; BAA36510.1; -  
 DR EMBL; AB008458; BAA36508.1; -  
 DR EMBL; AB008459; BAA36509.1; -

DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carri\_3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 88.5%; Score 1374.5; DB 13; Length 298;  
 Best Local Similarity 86.2%; Pred. No. 1.9e-120;  
 Matches 257; Conservative 24; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHMSFLDPLAGAAVAASKTAVAPIERVKLLLOVQHSKQISAEKQYGIIDCVR 60  
 Db 1 MTDAAISPAKDFLAGAAVAASKTAVAPIERVKLLLOVQHSKQITADKQYGIIDCVR 60  
 Qy 61 IPKQGFSLFWRGMLAVIRFFPTQALNFAFKDKYKQLFLGVDRHKOFWRYFAGNLASG 120  
 Db 61 IPKQGFSLFWRGMLAVIRFFPTQALNFAFKDKYKQLFLGVDRHKOFWRYFAGNLASG 120  
 Qy 61 IPKQGFSLFWRGMLAVIRFFPTQALNFAFKDKYKQLFLGVDRHKOFWRYFAGNLASG 120  
 Db 61 IPKQGFSLFWRGMLAVIRFFPTQALNFAFKDKYKQLFLGVDRHKOFWRYFAGNLASG 120  
 Qy 121 GAAGATSLCFYYPDPARTRLAADVGR-AQREPHGLDCCIIFKPSDGLKGLYQGFNV 179  
 Db 121 GAAGATSLCFYYPDPARTRLAADVGR-AQREPHGLDCCIIFKPSDGLKGLYQGFNV 179  
 Qy 121 GAAGATSLCFYYPDPARTRLAADVGR-AQREPHGLDCCIIFKPSDGLKGLYQGFNV 180  
 Db 121 GAAGATSLCFYYPDPARTRLAADVGR-AQREPHGLDCCIIFKPSDGLKGLYQGFNV 180  
 Qy 180 VGGIIIVRAAYFGYDTAKGMLPDPKXVHIFVSMIAQSTAVAGLLSYPPDTYRRMM 239  
 Db 180 VGGIIIVRAAYFGYDTAKGMLPDPKXVHIFVSMIAQSTAVAGLLSYPPDTYRRMM 239  
 Qy 181 VGGIIIVRAAYFGYDTAKGMLPDPKXVHIFVSMIAQSTAVAGLLSYPPDTYRRMM 240  
 Db 181 VGGIIIVRAAYFGYDTAKGMLPDPKXVHIFVSMIAQSTAVAGLLSYPPDTYRRMM 240  
 Qy 240 QSGRKGADIMTYGVDCWCKRIAKDEGAKAFKAGMSVNLKGAFVLVLYDEIKKYV 297  
 Db 241 QSGRKGADIMTYGVDCWCKRIAKDEGAKAFKAGMSVNLKGAFVLVLYDEIKKYV 298

## RESULT 9

Q919M9 PRELIMINARY; PRT; 298 AA.  
 AC Q919M9;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Adenine nucleotide translocase.  
 OS Acanthamoeba (Acanthamoeba).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX Crawford M.J., Khosrowshahian F., Varmuza S.L., Liverage R.A.;  
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and  
 Dynamic Patterns of Expression During Development.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AF21347; AAF63471.1; -  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carri\_3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 88.0%; Score 1366.5; DB 13; Length 298;  
 Best Local Similarity 86.2%; Pred. No. 1.1e-119;  
 Matches 257; Conservative 23; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MGDHMSFLDPLAGAAVAASKTAVAPIERVKLLLOVQHSKQISAEKQYGIIDCVR 60  
 Db 1 MGDHMSFLDPLAGAAVAASKTAVAPIERVKLLLOVQHSKQISAEKQYGIIDCVR 60

Db 1 MTDAAISPAKDFLAGVAAVAAISKTAVAPIERVKLLQVOHASKOITADKHGIMDCVVR 60  
 Qy 61 IPKQGFSPFRGNLANVIRFPYQALNFAFKDKYKOLFLGVDVHRHQFMRYPAGNLASG 120  
 Db 61 IPKQGFSPFRGNLANVIRFPYQALNFAFKDKYKOLFLGVDVHRHQFMRYPAGNLASG 120  
 Qy 121 GAAGATSLCFYYPPLDFATRLAADVGRRA-QREFHGLDCCIIFKPSDGLRGLYOGFNVS 179  
 Db 121 GAAGATSLCFYYPPLDFATRLAADVGRRA-QREFHGLDCCIIFKPSDGLRGLYOGFNVS 180  
 Qy 180 VQGIITRYAAVFGYVDIAKGMPLDPKKNVHIFVSMIAOSVTAVALGLSYPPDYVRRMM 239  
 Db 181 VQGIITRYAAVFGYVDIAKGMPLDPKKNVHIFVSMIAOSVTAVALGLSYPPDYVRRMM 240  
 Qy 240 QSGRKGADIMYTGVDICWRKIAKDEGAKAFKAGMSNVLKRMGCAFVLYLDEIKKYV 297  
 Db 241 QSGRKGADIMYTGVDICWRKIAKDEGAKAFKAGMSNVLKRMGCAFVLYLDEIKKYV 298

## RESULT 10

Q95VX4 PRELIMINARY; PRT; 299 AA.  
 ID Q95VX4  
 AC Q95VX4  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE ADP-ATP translocator.  
 OS Bthmoticigmus rubripes.  
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;  
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Bthmoticigmus.  
 NCBI\_Taxid=62613;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Burnell J.N.;  
 RT "Nucleotide sequence of an ADP-ATP translocator of Bthmoticigmus  
 rubripes.";  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF401758; AAL02100.1; -  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR02067; Mit\_carrier.  
 DR Pfam; PF00153; mito\_carrier; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 SQ SEQUENCE 299 AA; 33037 MW; 3C3BGB26E7C3CE CRC64;

Query Match 80.2%; Score 1245.5; DB 5; Length 299;  
 Best Local Similarity 80.3%; Pred. No. 2.3e-108;  
 Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

Qy 5 AWSFLKDFLAGVAAVAAVSKTAVAPIERVKLLQVOHASKOISAKOYKGIIDCVVRIPKE 64  
 Db 5 AWSFLKDFLAGVAAVAAVSKTAVAPIERVKLLQVOHASKOISAKOYKGIIDCVVRIPKE 64  
 Qy 65 QGFLSPFRGNLANVIRFPYQALNFAFKDKYKOLFLGVDVHRHQFMRYPAGNLASGAG 124  
 Db 65 QGFLSPFRGNLANVIRFPYQALNFAFKDKYKOLFLGVDVHRHQFMRYPAGNLASGAG 124  
 Qy 125 ATSLCFYYPPLDFATRLAADVGR-RAQREFHGLDCCIIFKPSDGLRGLYOGFNVSQGI 183  
 Db 125 ATSLCFYYPPLDFATRLAADVGR-RAQREFHGLDCCIIFKPSDGLRGLYOGFNVSQGI 184  
 Qy 184 IITYAAVFGYVDIAKGMPLDPKKNVHIFVSMIAOSVTAVALGLSYPPDYVRRMMOSGR 243  
 Db 185 IITYAAVFGYVDIAKGMPLDPKKNVHIFVSMIAOSVTAVALGLSYPPDYVRRMMOSGR 244  
 Qy 244 KGADIMYTGVDICWRKIAKDEGAKAFKAGMSNVLKRMGCAFVLYLDEIKKYV 297  
 Db 245 KGADIMYTGVDICWRKIAKDEGAKAFKAGMSNVLKRMGCAFVLYLDEIKKYV 298

RESULT 11  
 Q9NHWS PRELIMINARY; PRT; 300 AA.

AC Q9NHWS;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE ADP/ATP translocator.  
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Lucilia.  
 NCBI\_Taxid=7375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=SS mal seeking;  
 RT "A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AF218587; AF32322.1; -  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR02067; Mit\_carrier.  
 DR Pfam; PF00153; mito\_carrier; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 300 AA; 33036 MW; 5459DFOEA0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;  
 Best Local Similarity 78.7%; Pred. No. 5.6e-108;  
 Matches 236; Conservative 25; Mismatches 36; Indels 3; Gaps 1;

Qy 1 MGDA---WSFLKDFLAGVAAVAAVSKTAVAPIERVKLLQVOHASKOISAKOYKGIIDC 57  
 Db 1 MGDAADPLGVDKDFALGSAVSKTAVAPIERVKLLQVOHASKOISAKOYKGIIDC 60  
 Qy 58 VVRIPKQGFSPFRGNLANVIRFPYQALNFAFKDKYKOLFLGVDVHRHQFMRYPAGNL 117  
 Db 61 FVRIPKQGFSPFRGNLANVIRFPYQALNFAFKDKYKOLFLGVDVHRHQFMRYPAGNL 120  
 Qy 118 ASGGAATSLCFYYPPLDFATRLAADVGRRAQREFHGLDCCIIFKPSDGLRGLYOGFN 177  
 Db 121 ASGGAATSLCFYYPPLDFATRLAADVGRRAQREFHGLDCCIIFKPSDGLRGLYOGFN 180  
 Qy 178 VSVQGIITRYAAVFGYVDIAKGMPLDPKKNVHIFVSMIAOSVTAVALGLSYPPDYVRRM 237  
 Db 181 VSVQGIITRYAAVFGYVDIAKGMPLDPKKNVHIFVSMIAOSVTAVALGLSYPPDYVRRM 240  
 Qy 238 MMOSGRKADIMYTGVDICWRKIAKDEGAKAFKAGMSNVLKRMGCAFVLYLDEIKKYV 297  
 Db 241 MMOSGRKADIMYTGVDICWRKIAKDEGAKAFKAGMSNVLKRMGCAFVLYLDEIKKYV 300

## RESULT 12

Q8IRAO PRELIMINARY; PRT; 312 AA.  
 ID Q8IRAO  
 AC Q8IRAO  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE CG16944-PC.  
 GN SRSB.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=2019606; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abell J.F., Agbayan A., An H.J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Botkova D., Botchan M.A., Bouck J., Brockett P., Broctier P.,  
 RA Buttle K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glaeser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jajall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,  
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Sider-Kimose I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassenaar D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodard, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,  
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of Drosophila melanogaster.";  
 RA Science 287:2185-2195(2000).

[2]  
 RA SEQUENCE FROM N.A.  
 RA Ceinlier S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Geocayne J.D., Amancides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon K.Y., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.F., Gary N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jajall M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouaneavong S., Peltman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RA "Sequencing of Drosophila melanogaster genome.";  
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.

[3]  
 RA SEQUENCE FROM N.A.  
 RA Mirra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hrddecky P., Huang X., Kaminker J.S., Prochot S.E., Smith C.D.,  
 RA Rudy J.L., Bergman C., Berman B., Carlson J.W., Ceinlier S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Seale S.M.J., Smith R., Shu S., Smutnick F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RA "Annotation of Drosophila melanogaster genome.";  
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.

[4]  
 RA SEQUENCE FROM N.A.  
 RA Adams M.D., Ceinlier S.E., Gibbs R.A., Rubin G.M., Venter J.C.;  
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.

[5]  
 RA SEQUENCE FROM N.A.

RA FlyBase;  
 RA Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AB003484; AAN09267.1; -  
 DR SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;

Query Match 79.9%; Score 1241; DB 5; Length 312;

Best Local Similarity 79.7%; Pred. No. 6-66-108;  
 Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;  
 QY 5 AMSFLKDLGAVAAVSKTAVPIERVKLLQVQHSKQISAEKQYKGIIDCVRIPE 64  
 DB 20 AVGVQDPADAGISAAVSKTAVPIERVKLLQVQHSKQISAEKQYKGIIDCVRIPE 79  
 QY 65 QGFLSPFRGNLANVIRFPPTALNPAFKDKKQFLGVDVNHKKQFWRPAGNLASGGAAG 124  
 DB 80 QGFSPFRGNLANVIRFPPTALNPAFKDKKQFLGVDVNHKKQFWRPAGNLASGGAAG 139  
 QY 125 ATSLCPVPLDPARTBLAADVGRABREPHGIDGCIIFKPSDGLRGLYOGFNVSVGII 184  
 DB 140 ATSLCPVPLDPARTBLAADVGRABREPHGIDGCIIFKPSDGLRGLYOGFNVSVGII 199  
 QY 185 IYRAAYFGVDTAKGMLPDPKNVHIVSWMIQSVTAVAGLLSYFPDTRRRMMQSGRK 244  
 DB 200 IYRAAYFGVDTAKGMLPDPKNVHIVSWMIQSVTAVAGLLSYFPDTRRRMMQSGRK 259  
 QY 245 GADIMTGTVDCKRIKADSGAKAFPKGMSNVLRGMAAVLVLYDEIKK 295  
 DB 260 ATEYIKNTLHCWNTIAKQEGTGAFFKGAFAFNILRGTAFLVLYDEIKK 310

## RESULT 13

ID Q91336 PRELIMINARY; PRT; 317 AA.  
 AC Q91336;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS Rana sylvatica (Wood frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxId=45436;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=97398141; PubMed=9256066;  
 RA Cal O., Greenway S.C., Storey K.B.;  
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene  
 in wood frogs under freezing stress.";  
 RL Biochim. Biophys. Acta 1353:69-78(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Cal O., Storey K.B.;  
 RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: U4832; AA97882.2; -  
 DR InterPro: IPR001993; Mitoch. carrier.  
 DR InterPro: IPR002067; Mit. carrier.  
 DR Pfam: PF00153; mito. carri. 3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PROSITE: PS00215; MITOCH\_CARRIER. 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 317 AA; 35005 MW; 5F6687ED8D5CEB72 CRC64;

Query Match 79.5%; Score 1234.5; DB 13; Length 317;  
 Best Local Similarity 85.7%; Pred. No. 2-76-107;  
 Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHAWFLKDLGAVAAVSKTAVPIERVKLLQVQHSKQISAEKQYKGIIDCVRIPE 60  
 DB 1 MTDAAASFADDFLAGVAAVSKTAVPIERVKLLQVQHSKQITADKQKGLMDCVRI 60  
 QY 61 IPKQGFSPFRGNLANVIRFPPTALNPAFKDKKQFLGVDVNHKKQFWRPAGNLASG 120  
 DB 61 IPKQGFSPFRGNLANVIRFPPTALNPAFKDKKQFLGVDVNHKKQFWRPAGNLASG 120  
 QY 121 GAAGTSLCPVPLDPARTBLAADVGRABREPHGIDGCIIFKPSDGLRGLYOGFNVSV 179

Db 121 GAAGATSLCFYVPLDPARTRLAADVGKAGREFFNGLDCLAKIFKSDGLKGLYQGFVNS 180  
 Qy 180 VGGIITRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAGSVNAVAGLLSPDPTVRRMM 239  
 Db 181 VGGIITRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAGSVNAVAGFSGSPDPTVRRMM 240  
 Qy 240 QSGRKGADIMYTGVDCKWKIAKDEGAKAPFK 271  
 Db 241 QSGRKGADIMYTGVDCKWKIAKDEGAKAPFK 272

## RESULT 14

044094 PRELIMINARY; PRT; 288 AA.  
 AC 044094  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE ADP/ATP translocase (Fragment).  
 GN SSB.  
 OS Drosophila subobscura (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7241;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;  
 RL Genetics 0:0-0(1997).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AF025799; AAB87883.1; -;  
 DR FLYBase; FBgn0023237; Dros\seeb.  
 DR InterPro; IPR001993; Mitoch\\_carrier.  
 DR InterPro; IPR002067; Mlt\\_carrier.  
 DR Pfam; PF00153; mltc\\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH CARRIER; 3.  
 KW Membrane; Repeat; Transmembrane; Transport.  
 FT NON TER 288  
 SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;  
 Best Local Similarity 79.6%; Pred. No. 1.6e-102;  
 Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

Qy 5 AWSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVRLPKE 64  
 Db 7 AIGFVKDFPAAGGISAAVSKTAVAPIERVKLLQVQHSKQISPDQYKGMVDCFRIPKE 66  
 Qy 65 QGFLSFWRGNLANIRYPTQALNPAFKDKYKQLFLGVDNHHKQFWRFFAGNLASGGAAG 124  
 Db 67 QGFSSFWRGNLANIRYPTQALNPAFKDKYKQVFLGVDNHTQFWRFFMGNLASGGAAG 126  
 Qy 125 ATSLCFYVPLDPARTRLAADVGRRAPREPHGLGDCIIRKPSDGLRGLYOGFNVSVGGII 184  
 Db 127 ATSLCFYVPLDPARTRLAADVGRRAPREPHGLGDCIIRKPSDGLRGLYOGFNVSVGGII 186  
 Qy 185 IYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAGSVNAVAGLLSPDPTVRRMMQSGRK 244  
 Db 187 IYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAGSVNAVAGLLSPDPTVRRMMQSGRK 245  
 Qy 245 GADIMYTGVDCKWKIAKDEGAKAPFKGANSNVLKGMGAFLV 288  
 Db 246 ATEIIVKNTLHCWGTIAKQEGT-AFFKGAFSNVLKGTGAFLV 288

## RESULT 15

044093 PRELIMINARY; PRT; 288 AA.  
 AC 044093  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

ADP/ATP translocase (Fragment).  
 SSB.  
 Drosophila pseudoobscura (Fruit fly).  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7237;  
 [1]  
 SEQUENCE FROM N.A.  
 Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;  
 Genetics 0:0-0(1997).  
 -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 EMBL; AF025798; AAB87883.1; -;  
 FLYBase; FBgn0023292; Dros\seeb.  
 InterPro; IPR001993; Mitoch\\_carrier.  
 InterPro; IPR002067; Mlt\\_carrier.  
 Pfam; PF00153; mltc\\_carr; 3.  
 PRINTS; PR00926; MITOCARRIER.  
 PROSITE; PS00215; MITOCH CARRIER; 3.  
 Membrane; Repeat; Transmembrane; Transport.  
 NON TER 288  
 SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;  
 Best Local Similarity 79.6%; Pred. No. 1.6e-102;  
 Matches 226; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

Qy 5 AWSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVRLPKE 64  
 Db 7 AIGFVKDFPAAGGISAAVSKTAVAPIERVKLLQVQHSKQISPDQYKGMVDCFRIPKE 66  
 Qy 65 QGFLSFWRGNLANIRYPTQALNPAFKDKYKQLFLGVDNHHKQFWRFFAGNLASGGAAG 124  
 Db 67 QGFSSFWRGNLANIRYPTQALNPAFKDKYKQVFLGVDNHTQFWRFFMGNLASGGAAG 126  
 Qy 125 ATSLCFYVPLDPARTRLAADVGRRAPREPHGLGDCIIRKPSDGLRGLYOGFNVSVGGII 184  
 Db 127 ATSLCFYVPLDPARTRLAADVGRRAPREPHGLGDCIIRKPSDGLRGLYOGFNVSVGGII 186  
 Qy 185 IYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAGSVNAVAGLLSPDPTVRRMMQSGRK 244  
 Db 187 IYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAGSVNAVAGLLSPDPTVRRMMQSGRK 245  
 Qy 245 GADIMYTGVDCKWKIAKDEGAKAPFKGANSNVLKGMGAFLV 288  
 Db 246 ATEIIVKNTLHCWGTIAKQEGT-AFFKGAFSNVLKGTGAFLV 288

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 Job time : 32.598 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:34:56 ; Search time 35.3729 Seconds  
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1337.197 Million cell updates/sec

Title: US-09-811-131-32

Sequence: 1 MTDALSRANDFLAGVVA.....LRNGCAFVLYVDEIKKYT 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1547	100.0	298	AAV71032	Human adenine nucl
2	1547	100.0	298	AAU01199	Human adenine nucl
3	1547	100.0	298	AAU10379	Human adenine nucl
4	1537	99.4	298	AAO18516	Human insulin rece
5	1454	94.0	298	AAV71033	Human adenine nucl
6	1454	94.0	298	AAAM39641	Human polypeptide
7	1454	94.0	298	AAU01200	Human adenine nucl
8	1454	94.0	298	AAU10380	Human adenine nucl
9	1454	94.0	323	AAAM41427	Human polypeptide

10	1417	91.6	325	22	ABG15423	Novel human diago
11	1411	91.2	298	19	AAAG6169	Anti protein. Mus
12	1409	91.1	293	21	ABU53219	Human metaboliem-a
13	1391.5	89.9	297	22	AAV71031	Human adenine nucl
14	1391.5	89.9	297	23	AAU01198	Human adenine nucl
15	1391.5	89.9	297	23	AAU10378	Human adenine nucl
16	1346	87.0	263	22	ABG27056	Novel human diago
17	1339	86.6	429	24	ABR41715	Human DITHP organe
18	1253.5	81.0	299	22	ABBE6082	Drosophila melanog
19	1253.5	81.0	299	22	ABBE7300	Drosophila melanog
20	1125.5	72.8	307	22	ABBS8380	Human metaboliem-a
21	1102	71.2	315	23	AAU01198	Human adenine nucl
22	1102	71.2	315	23	AAU01198	Human adenine nucl
23	988	63.9	228	23	ABP43205	Human TRICH-19 pro
24	923	59.7	222	23	ABP74106	Human TRICH SRQ ID
25	895.5	57.9	298	22	ABG18922	Novel human diago
26	792	51.2	484	22	ABG15422	Novel human diago
27	792	51.2	484	22	ABG27055	Novel human diago
28	779.5	50.4	301	23	ABP73357	Candida albicans e
29	747.5	48.3	346	21	AAAG6577	Arabidopsis thalia
30	747.5	48.3	346	21	AAAG37261	Arabidopsis thalia
31	747.5	48.3	346	21	AAAG37264	Arabidopsis thalia
32	747.5	48.3	346	21	AAAG37264	Arabidopsis thalia
33	747.5	48.3	363	21	AAAG36576	Arabidopsis thalia
34	747.5	48.3	363	21	AAAG37260	Arabidopsis thalia
35	747.5	48.3	363	21	AAAG37263	Arabidopsis thalia
36	747.5	48.3	363	21	AAAG38459	Arabidopsis thalia
37	747.5	48.3	381	21	AAAG36575	Arabidopsis thalia
38	747.5	48.3	381	21	AAAG37259	Arabidopsis thalia
39	747.5	48.3	381	21	AAAG37262	Arabidopsis thalia
40	747.5	48.3	381	21	AAAG38458	Arabidopsis thalia
41	747.5	48.3	992	21	AAAG38672	Arabidopsis thalia
42	747.5	48.3	1009	21	AAAG38671	Arabidopsis thalia
43	747.5	48.3	1027	21	AAAG38670	Arabidopsis thalia
44	746	48.2	379	24	ABP81267	Arabidopsis thalia
45	744.5	48.1	346	21	AAAG17731	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1	AAV71032	standard; Protein: 298 AA.
ID	AAV71032	
AC	AAV71032;	
DT	29-AUG-2000	(first entry)
DE	Human adenine nucleotide translocator ANT2.	
XX	Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;	
XX	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;	
XX	mitochondrial permeability transition; neuroprotective; neurotrophic;	
XX	antiparkinsonian; cytotatic; antidiabetic; anticonvulsant; neuroleptic;	
XX	antiprotic; cerebroprotective; therapeutic; screening; poriasis;	
XX	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
XX	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;	
XX	mitochondrial encephalopathy; lactic acidosis; stroke; MTD;	
XX	mitochondrial diabetes and deafness; hyperproliferative disorder;	
XX	myoclonic epilepsy red ragged fibre syndrome.	
OS	Homo sapiens.	
PN	WO200026370-A2.	
PD	11-MAY-2000.	
PF	03-NOV-1999;	99WO-US25883.
PR	03-NOV-1998;	98US-0185904.
PR	08-SEP-1999;	99US-0393441.

PA (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,  
PI Ghosh SS,  
XX MPI: 2000-365619/31.  
DR N-PSDB; AAD00520.

XX Recombinant construct encoding adenine nucleotide translocator  
PT polypeptide, useful e.g. in screening for potential therapeutic agents  
PT against mitochondrial disease -

XX Claim 45; Page 172-173; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator  
CC (ANT) proteins or ANT fusion proteins using recombinant expression  
CC constructs. ANT is a nuclear encoded protein and a major component of  
CC inner mitochondrial membrane. It mediates transport of adenosine  
CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
CC as an important molecular component of the mitochondrial permeability  
CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
CC or ligands that bind to, or interact with it. The ANT ligands are used to  
CC detect or isolate ANT in a biological sample, and therapeutically for  
CC regulating mitochondrial pore activity, for treating diseases associated  
CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
CC epilepsy red ragged fibre syndrome. The present sequence is an  
CC adenine nucleotide translocator ANT2 from human brain.

XX Sequence 298 AA;

Query Match 100.0%; Score 1547; DB 21; Length 298;  
Best Local Similarity 100.0%; Pred. No. 2.3e-154;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDFLAGGVAALAAISKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60  
DB 1 MTDAALSPAKDFLAGGVAALAAISKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60  
QY 61 IPKGEVLSFWRGNLANVIRYFPQALNFAFKDKTKKQIFLGVDVKRTQFWRYFAGNLASG 120  
DB 61 IPKGEVLSFWRGNLANVIRYFPQALNFAFKDKTKKQIFLGVDVKRTQFWRYFAGNLASG 120  
QY 121 GAAGATSLCFYYPIDFARTRLAADVGKAGARERFGDCLVKIKYSGIKGLVQGFNV 180  
DB 121 GAAGATSLCFYYPIDFARTRLAADVGKAGARERFGDCLVKIKYSGIKGLVQGFNV 180  
QY 181 VGGIITRAAYFGIYDRAKGLPDPKNTHTIVSNMIAQTVAVAGLTSYPEDTVRRMM 240  
DB 181 VGGIITRAAYFGIYDRAKGLPDPKNTHTIVSNMIAQTVAVAGLTSYPEDTVRRMM 240  
QY 241 QSGRKGTDIMYTGTLDCWRKIARDGEGKAFKFGKMSNVLRMGAFVLVDEIKK 298  
DB 241 QSGRKGTDIMYTGTLDCWRKIARDGEGKAFKFGKMSNVLRMGAFVLVDEIKK 298

RESULT 2  
AAU01199 standard; Protein; 298 AA.

AAU01199;

07-SEP-2001 (first entry)

Human adenine nucleotide translocator-2 (ANT-2) protein.

Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;  
mitochondrial permeability transition pore component; cell survival;  
mitochondrial core component; mitochondrial related disorder; cancer;  
Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX Homo sapiens.

XX WO200132876-A2.

XX 10-MAY-2001.

XX 03-NOV-2000; 2000WO-US30535.

XX 03-NOV-1999; 99US-0434354.

XX (MITO-) MITOKOR.

XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG,  
PI Velicelebi G, Davis RB,  
XX MPI: 2001-291054/30.  
DR N-PSDB; AAS05902.

XX New nucleic acid expression constructs, useful for screening for agents  
PT that alter mitochondrial permeability transition (MPT), comprises  
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
PT fused to energy transfer molecule -  
XX Disclosure; Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-2  
CC (ANT-2) protein. ANT proteins are mitochondrial permeability  
CC transition (MPT) pore components responsible for mediating transport  
CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
CC with other mitochondrial core components e.g. cyclophilins to  
CC regulate MPT. The present invention relates to a novel nucleic acid  
CC expression construct comprising a promoter operably linked to a  
CC polynucleotide encoding a mitochondrial pore component polypeptide  
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
CC (e.g. green fluorescent protein (GFP) or a FLAHS sequence). The novel  
CC expression construct can alter mitochondrial membrane permeability  
CC transition and/or alter the interaction between mitochondrial core  
CC components. The methods are useful for screening for agents that alter  
CC MPT and/or cell survival. These agents are useful for the prevention or  
CC treatment of diseases associated with altered mitochondrial function or  
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
CC mitochondrial encephalopathy, lactic acidosis, stroke,  
CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 298 AA;

Query Match 100.0%; Score 1547; DB 22; Length 298;  
Best Local Similarity 100.0%; Pred. No. 2.3e-154;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDFLAGGVAALAAISKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60  
DB 1 MTDAALSPAKDFLAGGVAALAAISKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60  
QY 61 IPKGEVLSFWRGNLANVIRYFPQALNFAFKDKTKKQIFLGVDVKRTQFWRYFAGNLASG 120  
DB 61 IPKGEVLSFWRGNLANVIRYFPQALNFAFKDKTKKQIFLGVDVKRTQFWRYFAGNLASG 120  
QY 121 GAAGATSLCFYYPIDFARTRLAADVGKAGARERFGDCLVKIKYSGIKGLVQGFNV 180  
DB 121 GAAGATSLCFYYPIDFARTRLAADVGKAGARERFGDCLVKIKYSGIKGLVQGFNV 180  
QY 181 VGGIITRAAYFGIYDRAKGLPDPKNTHTIVSNMIAQTVAVAGLTSYPEDTVRRMM 240  
DB 181 VGGIITRAAYFGIYDRAKGLPDPKNTHTIVSNMIAQTVAVAGLTSYPEDTVRRMM 240  
QY 241 QSGRKGTDIMYTGTLDCWRKIARDGEGKAFKFGKMSNVLRMGAFVLVDEIKK 298  
DB 241 QSGRKGTDIMYTGTLDCWRKIARDGEGKAFKFGKMSNVLRMGAFVLVDEIKK 298



RESULT 3  
AAU10379  
ID AAU10379 standard; Protein; 298 AA.  
XX  
AC AAU10379;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Human adenine nucleotide translocator 2 (ANT2).  
XX  
KM Human; adenine nucleotide translocator; ANT; SB;  
KW mitochondrial matrix protein.  
XX  
OS Homo sapiens.  
XX  
PN W0200185944-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 11-MAY-2001; 2001WO-US15416.  
XX  
PR 11-MAY-2000; 2000US-0569327.  
XX  
PS (MITO-) MITOKOR.  
XX  
PI Anderson CM, Davis RE, Clevenger W, Wiley SB, Miller SW, Szabo TR;  
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;  
DR WPI; 2002-055598/07.  
DR N-PSDB; AAS16689.  
XX  
PT Novel recombinant expression construct for producing adenine nucleotide  
PT translocator polypeptides, comprises a regulated promoter linked to  
PT nucleic acid encoding the polypeptide  
XX  
PS Claim 44; Fig 2; 147pp; English.  
XX  
CC The invention relates to a recombinant expression construct (I)  
CC comprising a regulated promoter operably linked to a nucleic acid  
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
CC proteins mediate the exchange of ATP synthesized in the mitochondrial  
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
CC culturing the host cell. (I) is also useful for targeting a polypeptide  
CC of interest to a mitochondrial membrane, where ANT polypeptide is  
CC expressed as a fusion protein with the polypeptide of interest.  
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
CC ligand is useful for determining the presence of an ANT polypeptide.  
CC ANT from a biological sample, where the ANT ligand is covalently or non-  
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
CC useful for identifying an agent that interacts with an ANT polypeptide.  
CC The present sequence represents the amino acid sequence of human ANT2.  
XX  
SQ Sequence 298 AA;  
Query Match 100.0%; Score 1547; DB 23; Length 298;  
Best Local Similarity 100.0%; Pred. No. 2.3e-154;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTDAALSPADDFLAGVAAAIKSTAVAPIERVKLLDVOHASKQITADKQKGIIDCVNR 60  
DB 1 MTDAALSPADDFLAGVAAAIKSTAVAPIERVKLLDVOHASKQITADKQKGIIDCVNR 60  
QY 1PKQEVLSFWKGMANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFMRYFPAAGNLASG 120  
DB 61 IPKQEVLSFWKGMANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFMRYFPAAGNLASG 120  
QY 121 GAAGATSLCFYYPIDFARTRIADVGAGAEERFRGLGDCIVTKYSDGKIGLYOGFNVS 180  
DB 121 GAAGATSLCFYYPIDFARTRIADVGAGAEERFRGLGDCIVTKYSDGKIGLYOGFNVS 180

QY 181 VGGIIIRAAVFGIYDPAKGLPDPKNTHTVISMWIAQTVAAGLTSYPEDTVRRMM 240  
DB 181 VGGIIIRAAVFGIYDPAKGLPDPKNTHTVISMWIAQTVAAGLTSYPEDTVRRMM 240  
QY 241 QSGRKGTDIMYTGTLDCWRKIADDEGKAPFKGAMSVNLKMGAPVLVYDEIKKTT 298  
DB 241 QSGRKGTDIMYTGTLDCWRKIADDEGKAPFKGAMSVNLKMGAPVLVYDEIKKTT 298  
RESULT 4  
AAO18516  
ID AAO18516 standard; Protein; 298 AA.  
XX  
AC AAO18516;  
XX  
DT 11-OCT-2002 (first entry)  
XX  
DE Human insulin receptor signaling modifier SEQ ID NO: 54.  
XX  
KM Human; insulin receptor signaling; insulin receptor signaling modifier;  
KW ISM; diabetes; metabolic syndrome; antidiabetic.  
XX  
OS Homo sapiens.  
XX  
PN W0200255664-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 11-JAN-2002; 2002WO-US01048.  
XX  
PR 12-JAN-2001; 2001US-261226P.  
PR 12-JAN-2001; 2001US-261303P.  
PR 12-JAN-2001; 2001US-261304P.  
PR 12-JAN-2001; 2001US-261335P.  
PR 12-JAN-2001; 2001US-261336P.  
PR 12-JAN-2001; 2001US-261361P.  
PR 12-JAN-2001; 2001US-261456P.  
PR 12-JAN-2001; 2001US-261457P.  
PR 12-JAN-2001; 2001US-261458P.  
PR 12-JAN-2001; 2001US-261459P.  
PR 12-JAN-2001; 2001US-261461P.  
PR 12-JAN-2001; 2001US-261518P.  
PR 12-JAN-2001; 2001US-261531P.  
PR 12-JAN-2001; 2001US-261532P.  
PR 12-JAN-2001; 2001US-261533P.  
PR 12-JAN-2001; 2001US-261589P.  
PR 12-JAN-2001; 2001US-261590P.  
PR 12-JAN-2001; 2001US-261694P.  
PR 12-JAN-2001; 2001US-261695P.  
PR 12-JAN-2001; 2001US-261697P.  
XX  
PA (EXEL-) EXELIXIS INC.  
XX  
PI Seidel-Dugan C, Ferguson KC, Kidd T;  
PI N-PSDB; AAL48635.  
XX  
DR WPI; 2002-599664/64.  
XX  
PT Identifying an insulin receptor signaling modulator, useful as drug  
PT targets for treating diabetes or metabolic disorders, comprises  
PT contacting an assay system comprising insulin receptor signaling  
PT modifiers with a test agent  
XX  
PS Disclosure; Page 160-161, 232pp; English.  
XX  
CC The present invention relates to a method of identifying a candidate  
CC insulin receptor (INR) signaling modulating agent, involving contacting  
CC an assay system comprising an insulin receptor signaling modifier (ISM)  
CC polypeptide or nucleic acid with a test agent, and detecting a test  
CC agent-biased activity of the assay system. The method is useful for  
CC identifying candidate INR signaling modulating agents. ISM genes may be  
CC used as drug targets for treatment of disorders related to INR signaling  
CC such as diabetes or metabolic syndrome. ISM nucleic acids and  
CC polypeptides are useful for identifying and testing agents that modulate

CC ISM function and for other applications related to the involvement of ISM  
 CC in INR signaling, and for identifying subjects having a predisposition to  
 CC such diseases associated with INR signaling. The present sequence is an  
 CC ISM protein described in the exemplification of the invention.

XX Sequence 298 AA;

Query Match 99.4%; Score 1537; DB 23; Length 298;  
 Best Local Similarity 99.3%; Pred. No. 2.6e-153;  
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDPLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYGIIDCVVR 60  
 DB 1 MTDAVSPAKDPLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYGIIDCVVR 60  
 QY 61 IPKQEVLSFWRGNLANVIRFFPTQALNFAFKDKKKQIFLGVDKRTQFWRYFAGNLASG 120  
 DB 61 IPKQGVLSFWRGNLANVIRFFPTQALNFAFKDKKKQIFLGVDKRTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYYPPLDPARTRLADVGKAGABERFRLGDDCLVKIKSDGIRGLYOGFVS 180  
 DB 121 GAAGATSLCFYYPPLDPARTRLADVGKAGABERFRLGDDCLVKIKSDGIRGLYOGFVS 180  
 QY 181 VQGIITRAAFRGYIDTAKGMLPDPKNTHTIVSMWIAQTVAVAGLTSYPPDYRRRRMM 240  
 DB 181 VQGIITRAAFRGYIDTAKGMLPDPKNTHTIVSMWIAQTVAVAGLTSYPPDYRRRRMM 240  
 QY 241 QSGRKGIDIMYTGTLDCWRKIARDGKGAFFKAGMSNVLRGGAFFVLVLYDEIKKT 298  
 DB 241 QSGRKGIDIMYTGTLDCWRKIARDGKGAFFKAGMSNVLRGGAFFVLVLYDEIKKT 298

# RESULT 5

ID AAY71033 standard; Protein; 298 AA.

AC AAY71033;

DT 29-AUG-2000 (first entry)

DE Human adenine nucleotide translocator ANT3.

XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;  
 KW adenosine triphosphate; adenosine triphosphate; apoptosis; MPT; cancer;  
 KW mitochondrial permeability transition; neuroprotective; nocitropic;  
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
 KW antiparkinsonian; neuroprotective; therapeutic; screening; peptidase;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
 KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.

OS WO200026370-A2.

PN 11-MAY-2000.

PD 03-NOV-1999; 99WO-US25883.

PR 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-00393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS;

XX MPI; 2000-365619/31.

XX DR N-PSDB; AAD00521.

XX Recombinant construct encoding adenine nucleotide translocator

PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease -

XX Claim 46; Page 173-174; 175pp; English.

CC The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression of  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, peptidase, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT3 from human brain.

XX Sequence 298 AA;

Query Match 94.0%; Score 1454; DB 21; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 1.4e-144;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDPLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYGIIDCVVR 60  
 DB 1 MTEQALSPAKDPLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYGIIDCVVR 60  
 QY 61 IPKQEVLSFWRGNLANVIRFFPTQALNFAFKDKKKQIFLGVDKRTQFWRYFAGNLASG 120  
 DB 61 IPKQGVLSFWRGNLANVIRFFPTQALNFAFKDKKKQIFLGVDKRTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYYPPLDPARTRLADVGKAGABERFRLGDDCLVKIKSDGIRGLYOGFVS 180  
 DB 121 GAAGATSLCFYYPPLDPARTRLADVGKAGABERFRLGDDCLVKIKSDGIRGLYOGFVS 180  
 QY 181 VQGIITRAAFRGYIDTAKGMLPDPKNTHTIVSMWIAQTVAVAGLTSYPPDYRRRRMM 240  
 DB 181 VQGIITRAAFRGYIDTAKGMLPDPKNTHTIVSMWIAQTVAVAGLTSYPPDYRRRRMM 240  
 QY 241 QSGRKGIDIMYTGTLDCWRKIARDGKGAFFKAGMSNVLRGGAFFVLVLYDEIKKT 296  
 DB 241 QSGRKGIDIMYTGTLDCWRKIARDGKGAFFKAGMSNVLRGGAFFVLVLYDEIKKT 296

RESULT 6  
 ID AAM39641 standard; Protein; 298 AA.

AC AAM39641;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2786.

XX Human; nocitropic; immunosuppressant; cytosolic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX PD 26-JUL-2001.

PX	26-DEC-2000; 2000MO-US34263.
PR	21-JAN-2000; 2000US-0486725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0596042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
PA	(HYSB-) HYSB INC.
XX	
XX	Tang Y <sup>T</sup> , Liu C, Aundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
P1	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
P1	Zhao QA, Zhou P, Goodrich R, Dimanac RT;
XX	
DR	WPI: 2001-442253/47.
DR	N-PSTDB: AA158797.
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
PS	
XX	Example 4; SEQ ID NO 2786; 10078bp; English.
CC	The invention relates to human nucleic acids (AA157799-AA161369) and
CC	the encoded polypeptides (AAM38642-AAW42213) with nootropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Dreger Syndrome. Other uses include the
CC	utilisation of the activities such as: Immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC	and thromolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
SQ	specification.
XX	
XX	Sequence 298 AA;
Query Match	94.0%; Score 1454; DB 22; Length 298;
Best Local Similarity	92.6%; Pred. No. 1.4e-144;
Matches 274:	Conservative 13; Mismatches 9; Indels 0; Gaps 0
OY	1 MTDAALSPAKDFLAGVAANAISKTAVAPIERYKLLIQVHASKQITADKQYGIIDCVVR 60
Db	1 MTEQAISFAKDFLAGGIAAISIKTAVAPIERYKLLIQVHASKQIADKQYGIIDCVIR 60
OY	IPKEEVLSPFRGNANTYTRPPQTALNPAFEDKTKQIFLGVDNRTPQWRFFAENLASG 120
Db	61 IPKEGVLSFPMKGNANVTYRPPTALNPAFEDKTKQIFLGVDNRTPQWRFFAENLASG 120
OY	121 GAAGATSCFCFYPLDPARTRLAADVGKAEREFGELDCLVKIYKSDIGKLXOGFPNS 180
Db	121 GAAGATSCFCFYPLDPARTRLAADVGKSTEREFGLDCLVKITSDDIGKLXOGFSVS 180
OY	181 VGGIIITYRAAYFGIYDIAKGMLPDKNTHTIVSMNIAGOTVTNAVGLTSYPFDTRRRMM 240
Db	181 VGGIIITYRAAYFGVYDTAKGMPLDPKNTHTIVSMMIAGOTVTNAVGVSYPFDTVRRMMM 240
OY	241 OSGRGTDTIMTTGITLDCWRKILARDDEGGAFFFGANSNTLRMGGAFTVLYRYEIKK 296
Db	241 OSGRGADIMTYGITVDCWRKIIFRDEGGARFFFGANSNTLRMGGAFTVLYLDLKK 296
RESULT 7	
AAU01200	standard; Protein; 298 AA.
ID	AAU01200 standard; Protein; 298 AA.
XX	

Query Match	Best Local Similarity	92.6%	Score 1454;	DB 22;	Length 298;
Matches 274;	Conservative 13;	Mismatches 9;	Indels 0;	Gaps 0;	
DB	1	MTDAALSAKQPLAGVAAAIKSTKAVPIKSVKLLQVQHASKQITADKQYKGIIDCVR	60		
QY	1	MTDAALSAKQPLAGVAAAIKSTKAVPIKSVKLLQVQHASKQITADKQYKGIIDCVR	60		
DB	1	MTEQALISAKDPLAGGIAAIKSTKAVPIKSVKLLQVQHASKQITADKQYKGIIDCVR	60		
QY	61	IPKQEVLSFWRGNLANVIRYPTQALNFAKDKYKQITLQGVDRKRTQFWRYPAGNLASG	120		
DB	61	IPKQEVLSFWRGNLANVIRYPTQALNFAKDKYKQITLQGVDRKRTQFWRYPAGNLASG	120		
QY	121	GAAGATGTCFYPYLPDFAFTRILAAVQKGAARERFRGLDCLVKYIKSGIKGLYGFNVS	180		
DB	121	GAAGATGTCFYPYLPDFAFTRILAAVQKSGTEREFRGLDCLVKYIKSGIKGLYGFNVS	180		

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OY      181   YGGIITTYAAAFGIDVTAKGMLEDPENRTHIVISMMIAQTVLVAAGTSTPEPTVRRMMM    240
DB      181   VGGIIITYAARFVGVDITAKGLPDRNTHIVSMIAQTVALVAVGVSTPEPTVRRMMM    240
OY      241   QSGRKGTDMYTGTLDLCWRKILARDEGKAFFKGAMSNVLRGKAPFLVLYDEIKK    296
DB      241   OSGRGADIMYTGTVDLCWRKIIFRDEGKRFPFGAMSNVLRGGAFAVLVYLDELKK    296

RESULT 8
ID      AAU10380 standard; Protein; 298 AA.
AC      AAU10380;
XX      AAU10380;
DT      14-FEB-2002 (first entry)
DE      Human adenine nucleotide translocator 3 (ANT3).
KW      Human; adenine nucleotide translocator; ANT;
OS      mitochondrial matrix protein.
SS      Homo sapiens.
PN      WC020185944-A2.
PD      15-NOV-2001.
PE      11-MAY-2001, 2001WO-US15416.
PR      11-MAY-2000, 2000US-0569327.
PS      XZ
PA      (MITO-) MITOKOR.
PI      Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,
PI      Ghosh SS, Moos WH, Pei Y, Carroll AK;
XZ      WPI; 2002-055598/07.
DR      N-P5DB; AAS16690.
FT      Novel recombinant expression construct for producing adenine nucleotide
PT      translocator polypeptides, comprises a regulated promoter linked to
PT      nuclear acid encoding the polypeptide -
PS      Example 3; Fig 2; 147pp; English.

CC      The invention relates to a recombinant expression construct (I)
CC      comprising a regulated promoter operably linked to a nucleic acid
CC      encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC      proteins mediate the exchange of ATP synthesised in the mitochondrial
CC      matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC      ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC      culturing the host cell. (I) is also useful for targeting a polypeptide
CC      of interest to a mitochondrial membrane, where ANT polypeptide is
CC      expressed as a fusion protein with the polypeptide of interest.
CC      Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC      useful for identifying an agent that binds to an ANT polypeptide. ANT
CC      ligand is useful for determining the presence of an ANT polypeptide.
CC      preferably ANTI1, ANT2 or ANT3 in a biological sample and for isolating
CC      ANT from a biological sample, where the ANT ligand is covalently or non-
CC      covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC      useful for identifying an agent that interacts with an ANT polypeptide.
CC      The present sequence represents the amino acid sequence of human ANT3.

SO      Sequence          298 AA;

Query Match              94.0%; Score 1454; DB 23; Length 298;
Best Local Similarity    92.6%; Pred.No. 1.4e-14;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
```

Db	1	MTGQALISAAPKQFLAGIAAIAAISKTAVAPIERVKLLQVHAGSKQIAADQKQKGIIVDCIYR	60
Qy	61	IPKEQEVLSFMRGNLANVIRIFPTQALNFAFDOKTKQIITLGGYDKRTQTRRYAQNLAAG	120
Db	61	IPKEQGVLSFMRGNLANVIRIFPTQALNFAFDOKTKQIITLGGYDKRTQTRRYAQNLAAG	120
Qy	121	GAAGTSLICPVYPLDFAPTRILAADYGGKAGAREPGLGDLVKIYKSDGIKGLYQGFNV	180
Db	121	GAAGTSLICPVYPLDFAPTRILAADYGGKAGAREPGLGDLVKIYKSDGIKGLYQGFNV	180
Qy	181	VOGIIITRYAAVFGIYDTAKGMLPDPKNTHTIVISMMIAQTVTVAAGLTSYPFDIVRRMM	240
Db	181	VOGIIITRYAAVFGIYDTAKGMLPDPKNTHTIVISMMIAQTVTVAAGLTSYPFDIVRRMM	240
Qy	241	QSGRRKTDIMTGTITLDCWRKTIARDEGCKAFPFEGANSNVRMGGAVALVLYDEIRK	296
Db	241	QSGRRKADIMYTGIVDCWRKIFRDEGCKAFPFEGANSNVRMGGAVALVLYDEIRK	296
RESULT 9			
AA41427	ID	AA41427.standard; Protein, 323 AA.	
XX	AC	AA41427;	
XX	DT	22-OCT-2001 (first entry)	
XX	DE	Human polypeptide SRQ ID NO 6358.	
KW		Human, nocotropic; immunosuppressant; cyostatic; gene therapy; cancer;	
KW		peripheral nervous system; neuropathy; central nervous system; CNS;	
KW		Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;	
KW		amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW		chemokine; thrombolytic; drug screening; arthritis; inflammation;	
KW		leukaemia.	
OS		Homo sapiens.	
PN		WO200153312-A1.	
XX	PD	26-JUL-2001.	
PF		26-DEC-2000; 2000WO-US34263.	
XX	PR	21-JAN-2000; 2000US-0488725.	
XX	PR	25-APR-2000; 2000US-052317.	
XX	PR	09-JUL-2000; 2000US-0598042.	
XX	PR	19-JUL-2000; 2000US-0620312.	
XX	PR	03-AUG-2000; 2000US-0653450.	
XX	PR	14-SEP-2000; 2000US-0662191.	
XX	PR	19-OCT-2000; 2000US-0693036.	
XX	PR	29-NOV-2000; 2000US-0727344.	
PA		(HYSB-) HYSBQ INC.	
XX			
PI		Tang YF, Liu C, Aaurnd V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
PI		Wang Y, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;	
PI		Zhao QA, Zhou P, Goodrich R, Drmanac RT;	
XX		WPI, 2001-443253/47.	
DR		N-P8DB; AA160583.	
XX			
PT		Novel nucleic acids and polypeptides, useful for treating disorders	
PT		such as central nervous system injuries -	
XX			
PS		Example 2; SRQ ID NO 6358; 10078pp; English.	
XX			
CC		The invention relates to human nucleic acids (AA157798-AA161369) and	
CC		the encoded polypeptides (AA158642-AA162213) with nocotropic,	
CC		immunosuppressant and cyostatic activity. The polynucleotides are useful	
CC		in gene therapy. A composition containing a polypeptide or polynucleotide	
CC		of the invention may be used to treat diseases of the peripheral nervous	
CC		system, such as peripheral nervous injuries, peripheral neuropathy and	

CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

CC Sequence 323 AA;

CC Query Match 94.0%; Score 1454; DB 22; Length 323;

CC Best Local Similarity 92.6%; Pred. No. 1.6e-144;

CC Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVNR 60  
 DB 26 MTEQAIISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVNR 85  
 QY 61 IPKQGVLSFMRGNLANVIRFPFOALNPAFKDKTKQIFLGVDKRTQPMRYFAGNLASG 120  
 DB 86 IPKQGVLSFMRGNLANVIRFPFOALNPAFKDKTKQIFLGVDKRTQPMRYFAGNLASG 145  
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGAAGAREFRGLDCLVKIKYSDGIGLYQGFNV 180  
 DB 146 GAAGATSLCFVYPLDPARTRLAADVGAAGAREFRGLDCLVKIKYSDGIGLYQGFNV 205  
 QY 181 VQGIITVRAAYFGIYDPAKGLPDPKXTHIVISWMIQTVAVAGLTSYFEDTVRRMM 240  
 DB 206 VQGIITVRAAYFGIYDPAKGLPDPKXTHIVISWMIQTVAVAGLTSYFEDTVRRMM 265  
 QY 241 QSGRKGTDIMTTGTLDCWRKTLARDEGGAFFKGAWSNVLRMGAFVLVLYDEIKK 296  
 DB 266 QSGRKGADIMTGTLDCCWRKTLARDEGGAFFKGAWSNVLRMGAFVLVLYDEIKK 321

# RESULT 10

ABG15423 ID ABG15423 standard; Protein; 325 AA.

AC ABG15423;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #15414.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS79610.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

XX Claim 20; SEQ ID NO 45782; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

CC Sequence 325 AA;

CC Query Match 91.6%; Score 1417; DB 22; Length 325;

CC Best Local Similarity 92.7%; Pred. No. 1.3e-140;

CC Matches 280; Conservative 3; Mismatches 15; Indels 4; Gaps 3;

QY 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVNR 60  
 DB 24 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVNR 83  
 QY 61 IPKQGVLSFMRGNLANVIRFPFOALNPAFKDKTKQIFLGVDKRTQPMRYFAGNLASG 120  
 DB 84 IPKQGVLSFMRGNLANVIRFPFOALNPAFKDKTKQIFLGVDKRTQPMRYFAGNLASG 143  
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGAAGAREFRGLDCLVKIKYSDGIGLYQGFNV 180  
 DB 144 GAAGATSLCFVYPLDPARTRLAADVGAAGAREFRGLDCLVKIKYSDGIGLYQGFNV 203  
 QY 181 VQGIITVRAAYFGIYDPAKGLPDPKXTHIVISWMIQTVAVAGLTSYFEDTVRRMM 237  
 DB 204 VQGIITVRAAYFGIYDPAKGLPDPKXTHIVISWMIQTVAVAGLTSYFEDTVRRMM 263  
 QY 238 MMQSGRKGTDIMTTGTLDCWRKTLARDEGGAFFKGAWSNVLRMGAFVLVLYDEIKK 296  
 DB 264 MMQSGRKGTDIMTTGTLDCWRKTLARDEGGAFFKGAWSNVLRMGAFVLVLYDEIKK 323  
 QY 297 YT 298  
 DB 324 YT 325

# RESULT 11

AAM61169 ID AAM61169 standard; Protein; 298 AA.

AC AAM61169;

DT 28-SEP-1998 (first entry)

DE Ant1 protein.

XX Ant1; Adenine nucleotide translocator; cloning; screening;

KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;

KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;

KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;

OS Mus sp.

XX WO9819714-A1.  
 XX 14-MAY-1998.  
 XX  
 XX 31-OCT-1997, 97WO-US19882.  
 XX  
 XX 01-NOV-1996, 96US-0030017.  
 XX  
 XX (UYEM-) UNIV EMORY.  
 XX  
 XX Graham BC, Macgregor GR, Wallace DC,  
 XX WPI, 1998-286608/25.  
 XX N-PSDB, AAV36479.  
 XX  
 XX Mice lacking heart-muscle adenine nucleotide translocator protein -  
 XX useful as model for mitochondrial myopathy and hypertrophic  
 XX cardiomyopathy in animals and to test therapeutic compositions or  
 XX gene therapies  
 XX  
 XX PS Disclosure, Page 39-40; 61pp; English.  
 XX  
 CC The present sequence is the mouse Anti protein, the cDNA producing this  
 CC polypeptide is cloned by screening a mouse heart cDNA library with the  
 CC human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA  
 CC Tag deoxy terminator cycle sequencing. The Anti protein is encoded by  
 CC the Anti locus, a nuclear gene on chromosome 8. This protein is required  
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP  
 CC which can then be converted into ATP. An Anti homozygous mutant would  
 CC thus be defective in OXPHOS which results in disease in oxidative  
 CC metabolism dependent tissues. This mouse Anti homozygous mutant can be  
 CC used as a model system for fascioscapular humeral muscular dystrophy,  
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model  
 CC systems can be used to test possible therapeutic compounds which  
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane  
 CC independent of Anti.  
 CC  
 XX SQ Sequence 298 AA;

Query Match 91.2%; Score 1411; DB 19; Length 298;  
 Best Local Similarity 89.2%; Pred. No. 4.9e-140;  
 Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVVR 60  
 DB 1 MGDQALSLFKDFLAGGIAAASVKTAVPIERVKLLQVQHASKQISAEKQYGIIDCVVR 60  
 QY 61 IPKEGEVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFMRYPAGNLASG 120  
 DB 61 IPKEGEVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFMRYPAGNLASG 120  
 QY 121 GAAGATSLCFYVPLDFARTRLAADVGKAGAREEFGGLDCLVKIYKSDGIKGLYOGFNVSV 180  
 DB 121 GAAGATSLCFYVPLDFARTRLAADVGKAGAREEFGGLDCLVKIYKSDGIKGLYOGFNVSV 180  
 QY 181 VGGIIYYRAAYFGIYDTAKGMLPDPKXNTHIIVSMIACTTAVAGLISYPTVRRMM 240  
 DB 181 VGGIIYYRAAYFGIYDTAKGMLPDPKXNTHIIVSMIACTTAVAGLISYPTVRRMM 240  
 QY 241 QSGRGKDTIMTGTLLDCWRKIARDEGKAFKFGANSNVLKMGGAFLVLYLDEIKKY 297  
 DB 241 QSGRGKADIMYTGTLDCWRKIARDEGKAFKFGANSNVLKMGGAFLVLYLDEIKKY 297

## RESULT 12

ABUS3219  
 ID ABUS3219 standard; Protein; 293 AA.  
 XX  
 XX AC ABUS3219;  
 XX  
 XX DT 14-APR-2003 (first entry)  
 XX

DE Human metabolism-associated DKFZp35n12 homologue #1.  
 XX Human; gene therapy; vaccine; disease treatment; detection.  
 XX Homo sapiens.  
 XX WO200112659-A2.  
 XX  
 XX 22-FEB-2001.  
 XX  
 XX 18-AUG-2000; 2000WO-IB01496.  
 XX  
 XX 18-AUG-1999; 99US-0149499.  
 XX PR 28-SEP-1999; 99US-0156503.  
 XX  
 XX (GERU-) GERMAN HUMAN GENOME PROJECT.  
 XX  
 XX Wiemann S;  
 XX  
 XX WPI, 2001-327840/34.  
 XX  
 XX Nucleic acids having the sequences of clones isolated from libraries of  
 XX different human tissues, useful in recombinant DNA methodologies -  
 XX  
 XX PS Example III; Page 850; 1095pp; English.  
 XX  
 CC This invention describes novel polynucleotides and polypeptides isolated  
 CC from human cDNA libraries which can be used for gene therapy or in  
 CC vaccines. The polynucleotides of the invention and antibodies encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. The products of the  
 CC invention may also be used to identify modulators of expression and  
 CC activity and to down regulate expression and activity. The antibodies of  
 CC the invention may also be used as diagnostic agents for detecting the  
 CC presence of polypeptides in samples. This sequence represents a homologue  
 CC of a polypeptide described in the disclosure of the invention.  
 CC  
 XX SQ Sequence 293 AA;

Query Match 91.1%; Score 1409; DB 22; Length 293;  
 Best Local Similarity 90.1%; Pred. No. 7.7e-140;  
 Matches 264; Conservative 15; Mismatches 14; Indels 0; Gaps 0;  
 QY 5 ALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVVR 64  
 DB 1 ALSPKDFLAGGIAAASVKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVVR 60  
 QY 65 QEVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFMRYPAGNLASG 124  
 DB 61 QGFLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFMRYPAGNLASG 120  
 QY 125 ATSLCFYVPLDFARTRLAADVGKAGAREEFGGLDCLVKIYKSDGIKGLYOGFNVSV 184  
 DB 121 ATSLCFYVPLDFARTRLAADVGKAGAREEFGGLDCLVKIYKSDGIKGLYOGFNVSV 180  
 QY 185 IYRAAYFGIYDTAKGMLPDPKXNTHIIVSMIACTTAVAGLISYPTVRRMM 244  
 DB 181 IYRAAYFGIYDTAKGMLPDPKXNTHIIVSMIACTTAVAGLISYPTVRRMM 240  
 QY 245 KGTDTIMTGTLLDCWRKIARDEGKAFKFGANSNVLKMGGAFLVLYLDEIKKY 297  
 DB 241 KGADIMYTGTLDCWRKIARDEGKAFKFGANSNVLKMGGAFLVLYLDEIKKY 293

## RESULT 13

AA71031  
 ID AA71031 standard; Protein; 297 AA.  
 XX  
 XX AC AA71031;  
 XX  
 XX DT 29-AUG-2000 (first entry)  
 XX  
 XX Human adenine nucleotide translocator ANTI.

XX Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP;  
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
 KW mitochondrial permeability transition; neuroprotective; neurologic;  
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
 KW antiparkinsonian; cerebroprotective; therapeutic; screening; psoriasis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
 KW myoclonic epilepsy red ragged fibre syndrome.  
 OS Homo sapiens.  
 PN WO200026370-A2.  
 PD 11-MAY-2000.  
 PF 03-NOV-1999; 99WO-US25883.  
 PR 03-NOV-1998; 98US-0185904.  
 PR 08-SEP-1999; 99US-0393441.  
 XX (MITO-) MITOKOR.  
 PA Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR,  
 PI Ghosh S;  
 DR WPI; 2000-365619/31.  
 DR N-PSDB; AAD00519.  
 XX Recombinant construct encoding adenine nucleotide translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease -  
 XX Claim 44; Page 172; 175pp; English.  
 PS The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT1 from human brain.  
 XX  
 SQ Sequence 297 AA;  
 Query Match 89.9%; Score 1391.5; DB 21; Length 297;  
 Best Local Similarity 88.6%; Pred. No. 5.5e-138;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MTDAALSPAKDPLAGGVAALASTKAVAPRIERVKLLQVQHSKQITADKQKGIIDCVR 60  
 DB 1 MGDHAWSLKDPFLGAVAAVSKTAVAPRIERVKLLQVQHSKQISAKQYKGIIDCVR 60  
 QY 61 IPKQEVLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKRTQFMYFPAAGTASG 120  
 DB 61 IPKQGFSLFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKRTQFMYFPAAGTASG 120  
 QY 121 GAAGATSLCFYVPIIDFARTLADVGKAGAEERFGLDCLVKIKSDGINKLYGQFNVS 180  
 DB 121 GAAGATSLCFYVPIIDFARTLADVGRR-AQREFFGLDCLDKIKFKSDGINKLYGQFNVS 179

QY 181 VQGIITRAAYFGIYDTAKGMLPDPKNTHTLVISWMIQOTYAVAGLTSYEDTVRRMM 240  
 DB 180 VQGIITRAAYFGIYDTAKGMLPDPKNTHTLVISWMIQOTYAVAGLTSYEDTVRRMM 239  
 QY 241 QSGRKGTDIMWTGTLDCWRKIARDDEGKAPFKGAMSVNLKMGAPVLVYDEIKKY 297  
 DB 240 QSGRKGADIMWTGTDVDCWRKIARDDEGAKAPFKGAMSVNLKMGAPVLVYDEIKKY 296  
 RESULT 14  
 AAU01198  
 ID AAU01198 standard; Protein, 297 AA.  
 XX AC AAU01198;  
 XX DT 07-SEP-2001 (first entry)  
 XX DE Human adenine nucleotide translocator-1 (ANT-1) protein.  
 XX KW Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
 XX OS Homo sapiens.  
 XX PN WO200132876-A2.  
 XX PD 10-MAY-2001.  
 XX PF 03-NOV-2000; 2000WO-US30535.  
 XX PR 03-NOV-1999; 99US-0434354.  
 XX (MITO-) MITOKOR.  
 PA Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;  
 PI Velicelebi G, Davis RE;  
 DR WPI; 2001-291054/30.  
 DR N-PSDB; AAS05901.  
 XX New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 XX  
 PS Disclosure; Fig 2; 186pp; English.  
 CC The present sequence represents human adenine nucleotide translocator-1  
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability  
 CC translocator (MTP) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.  
 XX  
 SQ Sequence 297 AA;  
 Query Match 89.9%; Score 1391.5; DB 22; Length 297;  
 Best Local Similarity 88.6%; Pred. No. 5.5e-138;



Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKTAAPVPIERVKLLQVQHASKOITADKQYKGIIDCYVR 60  
 DB 1 MGDHMSFLKDFLAGVAAAVKTAAPVPIERVKLLQVQHASKOISAEKQYKGIIDCYVR 60

QY 61 IPKEGEVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQPMRYFAGNLASG 120  
 DB 61 IPKEGEVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQPMRYFAGNLASG 120

QY 121 GAAGATSLCFYYPPLDFAFTRLAADVGR-AQREFHGLDCLIKIKSDGLKGLYQGFNVS 180  
 DB 121 GAAGATSLCFYYPPLDFAFTRLAADVGR-AQREFHGLDCLIKIKSDGLKGLYQGFNVS 179

QY 181 VGGIITRYAAVFGYIDTAKGMLPDKNTHIVISNMIAQTVTAAGLTSYPTVRRRMM 240  
 DB 180 VGGIITRYAAVFGYIDTAKGMLPDKNTHIVISNMIAQTVTAAGLTSYPTVRRRMM 239

QY 241 QSGRKGTDIMYTGTLDCWRKILARDEGKAFKFGAMSNVLRGMGAFVLYLDEIKKY 297  
 DB 240 QSGRKGADIMYTGTLDCWRKILAKDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKY 296

RESULT 15  
 AAU10378 standard; Protein; 297 AA.

AC AAU10378;  
 XX 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 1 (ANT1).  
 XX Human; adenine nucleotide translocator; ANT;  
 KW mitochondrial matrix protein.  
 OS Homo sapiens.  
 XX WO200185944-A2.  
 XX 15-NOV-2001.  
 PD 11-MAY-2001; 2001WO-US15416.  
 PF 11-MAY-2001; 2000US-0569327.  
 XX 11-MAY-2000; 2000US-0569327.  
 PA (MITO-) MITOKOR.  
 XX Andersen CM, Davis RE, Cleverger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;  
 XX MPI; 2002-055598/07.  
 DR N-PSDB; AAS16688.

PT Novel recombinant expression construct for producing adenine nucleotide  
 translocator polypeptides, comprises a regulated promoter linked to  
 a nucleic acid encoding the polypeptide -  
 Claim 44; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating

CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT1.

XX  
 SQ Sequence 297 AA;  
 Query Match 89.9%; Score 1391.5; DB 23; Length 297;  
 Best Local Similarity 88.6%; Pred. No. 5.5e-138;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKTAAPVPIERVKLLQVQHASKOITADKQYKGIIDCYVR 60  
 DB 1 MGDHMSFLKDFLAGVAAAVKTAAPVPIERVKLLQVQHASKOISAEKQYKGIIDCYVR 60

QY 61 IPKEGEVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQPMRYFAGNLASG 120  
 DB 61 IPKEGEVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQPMRYFAGNLASG 120

QY 121 GAAGATSLCFYYPPLDFAFTRLAADVGR-AQREFHGLDCLIKIKSDGLKGLYQGFNVS 180  
 DB 121 GAAGATSLCFYYPPLDFAFTRLAADVGR-AQREFHGLDCLIKIKSDGLKGLYQGFNVS 179

QY 181 VGGIITRYAAVFGYIDTAKGMLPDKNTHIVISNMIAQTVTAAGLTSYPTVRRRMM 240  
 DB 180 VGGIITRYAAVFGYIDTAKGMLPDKNTHIVISNMIAQTVTAAGLTSYPTVRRRMM 239

QY 241 QSGRKGTDIMYTGTLDCWRKILARDEGKAFKFGAMSNVLRGMGAFVLYLDEIKKY 297  
 DB 240 QSGRKGADIMYTGTLDCWRKILAKDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKY 296

Search completed: December 18, 2003, 12:40:46  
 Job time : 35.3729 secs



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## OM protein - protein search, using sw model

Run on: December 18, 2003, 12:38:52 ; Search time 12.3471 Seconds

(without alignments)  
1021.178 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547  
Sequence: 1 MTDAALSPADFLAGVAA.....LRGMGAFLVLYDEIKKYT 298

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued Patents AA:\*

- 1: /cgm2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgm2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgm2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgm2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgm2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*
- 6: /cgm2\_6/ptodata/1/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	4	US-09-434-354-48
2	1454	94.0	298	4	US-09-434-354-49
3	1411	91.2	298	3	US-08-961-871-10
4	1391.5	89.9	297	4	US-09-434-354-47
5	302	19.5	469	4	US-09-996-243-289
6	301	19.5	469	3	US-09-188-930-339
7	301	19.5	469	4	US-09-312-283C-339
8	274	17.7	291	4	US-09-501-558-2
9	274	17.7	335	4	US-09-483-273-118
10	261.5	16.9	447	4	US-09-160-119-4
11	261.5	16.9	674	4	US-09-160-119-2
12	247	16.0	312	3	US-09-142-565-2
13	244.5	15.8	311	2	US-08-775-009-33
14	239.5	15.5	309	1	US-08-518-878B-51
15	239.5	15.5	309	2	US-08-807-861A-51
16	239.5	15.5	309	2	US-08-470-868A-51
17	239.5	15.5	309	3	US-09-210-681-51
18	239.5	15.5	309	3	US-08-946-719A-51
19	239.5	15.5	309	4	US-09-547-983-51
20	236.5	15.3	299	1	US-08-518-878B-56
21	236.5	15.3	299	2	US-08-470-868A-56
22	232.5	15.0	311	2	US-08-775-009-32
23	230.5	14.9	320	2	US-08-933-750C-12
24	230.5	14.9	320	3	US-09-234-613-12
25	227	14.7	308	2	US-08-937-466-2
26	227	14.7	308	2	US-09-172-528-2
27	227	14.7	308	3	US-09-318-199-2

28	227	14.7	308	3	US-09-503-579-2	Sequence 2, Appl1
29	223	14.4	432	2	US-08-937-466-4	Sequence 4, Appl1
30	223	14.4	432	2	US-08-172-528-4	Sequence 4, Appl1
31	223	14.4	432	3	US-09-318-199-4	Sequence 4, Appl1
32	219.5	14.2	432	3	US-09-503-579-4	Sequence 4, Appl1
33	218.5	14.1	303	1	US-08-294-522B-36	Sequence 36, Appl1
34	217.5	14.1	303	1	US-08-518-878B-37	Sequence 37, Appl1
35	217.5	14.1	303	2	US-08-807-861A-37	Sequence 37, Appl1
36	217.5	14.1	303	2	US-08-470-868A-37	Sequence 37, Appl1
37	217.5	14.1	303	3	US-09-210-681-37	Sequence 37, Appl1
38	217.5	14.1	303	3	US-08-946-719A-37	Sequence 37, Appl1
39	217.5	14.1	303	4	US-09-547-983-37	Sequence 37, Appl1
40	217.5	14.1	328	3	US-09-068-140A-15	Sequence 15, Appl1
41	191	12.3	256	2	US-08-937-466-6	Sequence 6, Appl1
42	190.5	12.3	256	2	US-08-172-528-6	Sequence 6, Appl1
43	190.5	12.3	256	3	US-09-318-199-6	Sequence 6, Appl1
44	190.5	12.3	256	3	US-09-503-579-6	Sequence 6, Appl1
45	190.5	12.3	256	3	US-09-503-579-6	Sequence 6, Appl1

## ALIGNMENTS

RESULT 1  
US-09-434-354-48  
Sequence 48, Application US/09434354Patent No. 6562563  
GENERAL INFORMATION:

Query Match 100.0%; Score 1547; DB 4; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.2e-169;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTDAALSPADFLAGVAAATSKTAVAPIERVKLLLOVQASKQITADKQYKGIIDCVR	60
DB	1	MTDAALSPADFLAGVAAATSKTAVAPIERVKLLLOVQASKQITADKQYKGIIDCVR	60
QY	61	IPKQEVLSFWRGNLAVIRFPQALNFAKDKYKQIFLGVNKRQPMWYPAAGTASG	120
DB	61	IPKQEVLSFWRGNLAVIRFPQALNFAKDKYKQIFLGVNKRQPMWYPAAGTASG	120
QY	121	GAAGATSLCFYPPDFAFTRLAADVGAQARERRGIDCLVYKSDGIGLYQGFVNS	180
DB	121	GAAGATSLCFYPPDFAFTRLAADVGAQARERRGIDCLVYKSDGIGLYQGFVNS	180
QY	181	VQGIITRAAIFGYYDAKGMPLDPKNTHTYISMMIAQTVAVAGLSYPPDYRRRRMM	240
DB	181	VQGIITRAAIFGYYDAKGMPLDPKNTHTYISMMIAQTVAVAGLSYPPDYRRRRMM	240
QY	241	QSGRGTIDIMVTGTLDCWRKIARDGGAFFKGAAMSVLRMGAFVLYVDEIKKYT	298
DB	241	QSGRGTIDIMVTGTLDCWRKIARDGGAFFKGAAMSVLRMGAFVLYVDEIKKYT	298

RESULT 2  
US-09-434-354-49  
Sequence 49, Application US/09434354  
Patent No. 6562563  
GENERAL INFORMATION:  
APPLICANT: Murphy, Anne N.  
APPLICANT: Clevenger, William  
APPLICANT: Wilev, Sandra Eileen  
APPLICANT: Andreyev, Alexander Y.  
APPLICANT: Frigert, Luciano G.  
APPLICANT: Velicelch, Gonul  
APPLICANT: Davis, Robert E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
FILE REFERENCE: 660088.433  
CURRENT APPLICATION NUMBER: US/09/434,354  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 49  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-434-354-49

Query Match 94.0%; Score 1454; DB 4; Length 298;  
Best Local Similarity 92.6%; Pred. No. 6.3e-159;  
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAAEFKADFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVR 60  
DB 1 MTEQGISAKDFLAGIAAIAIKSTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVR 60  
QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGRHQPMRYFAGNLASG 120  
DB 61 IPKEQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGRHQPMRYFAGNLASG 120  
QY 121 GAAAGTSCFYYPDPARTRLAADVKGAGAREFRGLDCLVKIYKSGDGIKGLYQGFVNS 180  
DB 121 GAAAGTSCFYYPDPARTRLAADVKGAGAREFRGLDCLVKIYKSGDGIKGLYQGFVNS 180  
QY 181 VGGIIRAAAYFGYDTRAKGMLPDPKNTHTIVISWIAQTVTAAGLTSYPPDTRRRMM 240  
DB 181 VGGIIRAAAYFGYDTRAKGMLPDPKNTHTIVISWIAQTVTAAGLTSYPPDTRRRMM 240  
QY 241 QSGRGTIDIMTGTLDCKRKIARDEGKAFPKGAMSNVLRGMGAFTVLVYDEIKY 296  
DB 241 QSGRGTIDIMTGTLDCKRKIARDEGKAFPKGAMSNVLRGMGAFTVLVYDEIKY 296

## RESULT 3

US-08-961-871-10  
Sequence 10, Application US/08961871  
Patent No. 6013858  
GENERAL INFORMATION:  
APPLICANT: Wallace, Douglas C.  
APPLICANT: Graham, Brett H.  
APPLICANT: Macgregor, Grant R.  
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine  
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,871  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/030,017  
FILING DATE: 01-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Feiber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 78-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
US-08-961-871-10

Query Match 91.2%; Score 1411; DB 3; Length 298;  
Best Local Similarity 89.2%; Pred. No. 5.6e-154;  
Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MTDAAEFKADFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVR 60  
DB 1 MGDQSLFKDPLFGIAAIAIKSTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVR 60  
QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGRHQPMRYFAGNLASG 120  
DB 61 IPKEQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGRHQPMRYFAGNLASG 120  
QY 121 GAAAGTSCFYYPDPARTRLAADVKGAGAREFRGLDCLVKIYKSGDGIKGLYQGFVNS 180  
DB 121 GAAAGTSCFYYPDPARTRLAADVKGAGAREFRGLDCLVKIYKSGDGIKGLYQGFVNS 180  
QY 181 VGGIIRAAAYFGYDTRAKGMLPDPKNTHTIVISWIAQTVTAAGLTSYPPDTRRRMM 240  
DB 181 VGGIIRAAAYFGYDTRAKGMLPDPKNTHTIVISWIAQTVTAAGLTSYPPDTRRRMM 240  
QY 241 QSGRGTIDIMTGTLDCKRKIARDEGKAFPKGAMSNVLRGMGAFTVLVYDEIKY 297  
DB 241 QSGRGTIDIMTGTLDCKRKIARDEGKAFPKGAMSNVLRGMGAFTVLVYDEIKY 297

## RESULT 4

US-09-434-354-47  
Sequence 47, Application US/09434354  
Patent No. 6562563  
GENERAL INFORMATION:  
APPLICANT: Murphy, Anne N.  
APPLICANT: Clevenger, William  
APPLICANT: Wilev, Sandra Eileen  
APPLICANT: Andreyev, Alexander Y.  
APPLICANT: Frigert, Luciano G.  
APPLICANT: Velicelch, Gonul  
APPLICANT: Davis, Robert E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
FILE REFERENCE: 660088.433  
CURRENT APPLICATION NUMBER: US/09/434,354  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Homo sapien

US-09-434-354-47

Query Match 89.9%; Score 1391.5; DB 4; Length 297;  
 Best Local Similarity 88.6%; Pred. NO. 9.8e-152;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDAALSPAKDFLAGVAAAIKSTAVADIERVKLLQVQHASKQITADKOYKGIIDCVR 60  
 DB 1 MGDHMSFLKDFLNGAVAAVSKTAVADIERVKLLQVQHASKQISAKQYKGIIDCVR 60  
 QY 61 IPKGEVLSFMRGNLANIRYPTQALNPAFKDKTKQIFLGGVDKRTQFMRYPAGNLASG 120  
 DB 61 IPKGEVLSFMRGNLANIRYPTQALNPAFKDKTKQIFLGGVDKRTQFMRYPAGNLASG 120  
 QY 121 GAAGATSLCFYPLDPFARTPLAADVKGAGAREPFGLDGCVKIKYKSGIIGLVQGFVNS 180  
 DB 121 GAAGATSLCFYPLDPFARTPLAADVKGAGAREPFGLDGCVKIKYKSGIIGLVQGFVNS 179  
 QY 181 VQGIIVRAAYFGYVDIAKGMIPDKNTHIVISWMAQVTAVAGLTSYPPDTRRRMM 240  
 DB 180 VQGIIVRAAYFGYVDIAKGMIPDKNTHIVISWMAQVTAVAGLTSYPPDTRRRMM 239  
 QY 241 QSGRKVDIMTGTILDCRKXIAKDEGGKAFKGMANSVLRGMAFVLVYDEIKKY 297  
 DB 240 QSGRKVDIMTGTILDCRKXIAKDEGGKAFKGMANSVLRGMAFVLVYDEIKKY 296

RESULT 5  
 US-09-996-243-289  
 Sequence 289, Application US/09996243  
 Patent NO. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bostein, David  
 APPLICANT: Deenoyers, Luc  
 APPLICANT: Batcon, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerder, Hanspeter  
 APPLICANT: Gottlieb, Mary B.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas P.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C13  
 CURRENT APPLICATION NUMBER: US/09/996,243  
 PRIOR FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/087106  
 PRIOR FILING DATE: 1998-05-28  
 PRIOR APPLICATION NUMBER: 60/087607  
 PRIOR FILING DATE: 1998-06-02  
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 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087759  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087827  
 PRIOR FILING DATE: 1998-06-03  
 PRIOR APPLICATION NUMBER: 60/088021  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088025  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088026  
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 PRIOR FILING DATE: 1998-06-10  
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 PRIOR FILING DATE: 1998-06-11  
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 PRIOR FILING DATE: 1998-06-16  
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 PRIOR FILING DATE: 1998-06-16  
 PRIOR APPLICATION NUMBER: 60/089514  
 PRIOR FILING DATE: 1998-06-16  
 PRIOR APPLICATION NUMBER: 60/089532  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089538  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089598

PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
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PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
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PRIOR FILING DATE: 1998-06-22  
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PRIOR FILING DATE: 1998-06-22  
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PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02.

PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 19.5%; Score 302; DB 4; Length 469;  
Best Local Similarity 29.1%; Pred. No. 5.4e-26;  
Matches 86; Conservative 60; Mismatches 118; Indels 32; Gaps 11;

QY 10 KDLAAGVAAIAISTAVPIERVKLLQVQASKOITADKOYKGIIDCV---RIPPEQ 65  
DB 188 RHVAGGAGAVSRTCTPDLRLKVMQV-HASR-----SNMGIYVGFQIMREGARS 241  
QY 70 FWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKTQFWRYFAGNLAGAGATSLC 129  
DB 242 LMRGGINVLKIAESAIKFMAVEQIKR--LVGSDQET---LRHERLVAGSLAGAIQS 296  
QY 130 FVPLDFAKRTLADVGAEREREGDCLVITKSDGIKGLYQGFNVVQGIITRA 189  
DB 297 SIYMEVLTKTMA--LRRTG---QYSGMLDARRILAREGVAAFKGYVPPNMLGITPYAG 351  
QY 190 AVFGIYDTAKGM-----LPDPKNTIIVISWMIQTVTAAG-LTSYPPDTVRRMM 240  
DB 352 IDLAVETLNKAMLOHVAVNSADP-----VVLACGMSSTCGLASPYLALVRRMQA 407  
QY 241 QSGRGTDIMYGTIDCWRKTIARDEGKAFKFGKMSNVLKMGAFV-LVLYDEIX 295  
DB 408 QASIEGAEVETMSI--FKHILRTGAGFLYGLAPNFMKIVPAVSIYVYVENIK 461

RESULT 6  
US-09-188-930-339  
Sequence 339, Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murlison, James Greg  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
FILE REFERENCE: 11000.1011c1  
CURRENT APPLICATION NUMBER: US/09/188, 930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 339  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Mouse  
US-09-188-930-339

Query Match 19.5%; Score 301; DB 3; Length 469;  
Best Local Similarity 28.4%; Pred. No. 7e-26;  
Matches 86; Conservative 62; Mismatches 109; Indels 46; Gaps 12;  
QY 10 KDLAAGVAAIAISTAVPIERVKLLQVQASKOITADKOYKGIIDCV---RIPPEQ 65  
DB 188 RHVAGGAGAVSRTCTPDLRLKVMQV-HASRNNM-----CIVGFGTQIMREG 237  
QY 66 EVLSFWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKTQFWRYFAGNLAGAGAA 125  
DB 238 GAKSIMGNGINVLKIAESAIKFMAVEQIKR--LVGSDQET---LRHERLVAGSLAGA 292  
QY 126 TSLCFVPLDFAKRTLADVGAEREREGDCLVITKSDGIKGLYQGFNVVQGIIT 185

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Db      293  IAGSSIVMEVLTAKTMA--LRKTYG---QYSGMLDCARRILAKEGVAFAFYKGIIPMLGII 347
Qy      186  IYRAVFGIYDTAKGMLDPKNTHT-----VISMIAQVTVAVAG--LTSYPRDT 233
Db      348  PYAGIDLAVETL-----KNTWLORYAVNSADPGVVLACGTTISSTCCQLASYPAL 400
Qy      234  VRRRMOMSGRKGTIDIMYTGTLDCWKRIARDEGKAFPKGAMSNLRGMAFV--LVLYD 292
Db      401  VRTNRQAQASIEGAEVYMSL--FKQILRTGAGAGLRLGALPFPNMKVIPIAVSISVYVE 458
Qy      293  EIK 295
Db      459  NLK 461

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RESULT 7
US-09-312-283C-339
; Sequence 339, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for their Use
; FILE REFERENCE: 11000.1011C2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-339

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Query Match      19.5%; Score 301; DB 4; Length 469;
Best Local Similarity 28.4%; Pred. No. 7e-26;
Matches 86; Conservative 62; Mismatches 109; Indels 46; Gaps 12;

Qy      10  KDPLAGVAAAIISKAVAPIERVKLLQVHASKQITADKQYGIIDCV---RIPREQ 65
Db      188  RHLVAGGAGAVSRCTAPLDLKVLMQV--HASRSNNM-----CIVGGFTQIMREG 237
Qy      66  EVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGGAAGA 125
Db      238  GAKSIRMRNGINVLKIAPESAIKFPAVQMKR--LVGSDQET---LRTHRLVAGSLAGA 292
Qy      126  TSLCFVYPLDPARTRLADVGAKGAEERFRLGDCLVKIYKSDGIKGLYOGFNVSVOGII 185
Db      293  IAGSSIVMEVLTAKTMA--LRKTYG---QYSGMLDCARRILAKEGVAFAFYKGIIPMLGII 347
Qy      186  IYRAVFGIYDTAKGMLDPKNTHT-----VISMIAQVTVAVAG--LTSYPRDT 233
Db      348  PYAGIDLAVETL-----KNTWLORYAVNSADPGVVLACGTTISSTCCQLASYPAL 400
Qy      234  VRRRMOMSGRKGTIDIMYTGTLDCWKRIARDEGKAFPKGAMSNLRGMAFV--LVLYD 292
Db      401  VRTNRQAQASIEGAEVYMSL--FKQILRTGAGAGLRLGALPFPNMKVIPIAVSISVYVE 458
Qy      293  EIK 295
Db      459  NLK 461

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RESULT 8
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:

```

```

; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Zachur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
; FILE REFERENCE: LEX-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2

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Query Match      17.7%; Score 274; DB 4; Length 291;
Best Local Similarity 27.8%; Pred. No. 4.3e-23;
Matches 85; Conservative 55; Mismatches 134; Indels 32; Gaps 9;

Qy      4  AALSPADFLAGVAAAIISKAVAPIERVKLLQVHAS-----KQITADKQYGIIDCV 58
Db      2  SALNW-KPFGYGGIASITABCGTEPIDLTTRLQIQCGTDAKPEI-----RYRGMLHAL 56
Qy      59  VRIKBOEVLSPWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLA 118
Db      57  VRIKBOEVLKALVSGIAPAMLRQASGTIKIGYQSLKLPTEPRDET-----LPINVI 111
Qy      119  SGGAAGATSLCFVYPLDPARTRLADVGAKGAEERFRLGDCLVKIYKSDGIKGLYOGFN 178
Db      112  CGILSGVISTIANPTLVAKIRMQASNTIOG-----GMGNFNNITQOEGTRGLMKGVS 166
Qy      179  VSVQGIITIRAYAGIYDTAK-----GMLDPKNTHTVISMIAQVTVAVAGLTSYPRD 232
Db      167  LTAQRAAIWGVSLPVVDITKHLILSLMGDFVTYHFLSSF-----TCGLAGALASNPVD 222
Qy      233  TVRRBMOMSG-RKGTIDIMYTGTLDCWKRIARDEGKAFPKGAMSNLR--GMGAFLVYL 290
Db      223  VRTNRQAQASIEGAEVYMSL--FKQILRTGAGAGLRLGALPFPNMKVIPIAVSISVYVE 282
Qy      291  YDEIKK 296
Db      283  YEOLK 288

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RESULT 9
US-09-482-273-118
; Sequence 118, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (335)

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OTHER INFORMATION: Xaa equals stop translation  
US-09-482-273-118

Query Match 17.7%; Score 274; DB 4; Length 335;  
Best Local Similarity 28.1%; Pred. No. 5,4e-23;  
Matches 84; Conservative 51; Mismatches 134; Indels 30; Gaps 8;

QY 10 KDLAAGVAAAIKSTAVAPIERVELLQVQHAS-----KQITADKQYKIIDCVRIKPE 64  
DB 51 KPEVVGGLASIVAEFEFTFVDTLTKTLQVQOSIDARFKEI-----KYRGMFHALFRICKE 106  
QY 65 QEVLSFPMGNLANVRYEPTQALNFAFKQKQIFLGVDKRTQFRRYAGNLASGAGAG 124  
DB 107 EGVIALYSGIADPALRQASVGTIKIGIYSLRLFEKREDEPT-----LLINMIGSVSG 161  
QY 125 ATSLCFVYPLDPAFRLADVKGAGAREFRGLDCLVYIKYSDGKGLYOGFNVSVQGI 184  
DB 162 VASSTIANPTDVLKRMQO-----GSLFGSGMIGS-FIDITYOEGTRGLMRGVPTAQRA 216  
QY 185 IYRAAYFGIYDTAK-----GMLDPPKXTHIVISWMLAQVTAVAGLTSYFPDTRRM 238  
DB 217 AIVGVEELPVYDITKKHLILSGMWGDTLTHFVSSF-----TCGLAGALASNPDVVRTRM 272  
QY 239 MMQSGRKGDIMYTGTLDCKRKIADDEGKAFPKGAMSVNR-GMGCAFVLVYDEIKK 296  
DB 273 MMQRAIVGHVDLYKGTVDGILKMMKREGFALYKGFPMWMLKLGPMNIIFFITYEOLKR 331

RESULT 10  
US-09-160-119-4  
Sequence 4, Application US/09160119A  
Patent No. 6316219  
GENERAL INFORMATION:  
APPLICANT: KRIEF, STEPHANE  
APPLICANT: SOUCHET, MICHEL  
APPLICANT: BRIL, ANTOINE  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GH-30985  
CURRENT APPLICATION NUMBER: US/09/160,119A  
CURRENT FILING DATE: 1998-09-24  
EARLIER APPLICATION NUMBER: EP 97402511.6  
EARLIER FILING DATE: 1997-10-23  
EARLIER APPLICATION NUMBER: EP 98401655.0  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 447  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-09-160-119-4

Query Match 16.9%; Score 261.5; DB 4; Length 447;  
Best Local Similarity 26.2%; Pred. No. 2.3e-21;  
Matches 77; Conservative 51; Mismatches 139; Indels 27; Gaps 7;

QY 12 FLAGVAAAIKSTAVAPIERVELLQVQHASKQITADKQYKIIDCVRIKPEQEVLSFW 71  
DB 104 FGLSVAGVAGTAVYPIDLVKTRMONGRSTGSPVGEIMYKNSPDCFKVLRYEGFGLY 163  
QY 72 RGNLANVIRYPTQALNFAFKQKQIFL---GGVDKRTQFRRYAGNLASGAGAGATSL 128  
DB 164 RGLLPOLLGVAPEKAIKLTVDVFRDKFMHKGVSVP-----LAAEIIAGGCGAGGSQV 215  
QY 129 CFVYPLDPAFRLADVKGAGAREFRGLDCLVYIKYSDGKGLYOGFNVSVQGI 188  
DB 216 IFPMLELVKIRLQV-----AGEITTPRVSALSVRDGLFPGIYKAKACFLRDI 269  
QY 189 AAYFGIYDTAKGMLDPPKXTHIVISWMLAQVTAVAGLTS---YFPDTRRMMSQGR 244  
DB 270 AIVFCYAHVYKASPNEDQVSPGSLILA---GALAGMPASLVTPADVIKTR--LQVAA 324  
QY 245 KGTIMTGTLDCKRKIADDEGKAFPKGAMSVNLRMGG-AFVLVLYDEIKKY 297

DB 325 RAGQTTYSVIDCPRKILREBGPALMKGAGARVRSSPQGVTLTYELLQRW 378

RESULT 11  
US-09-160-119-2  
Sequence 2, Application US/09160119A  
Patent No. 6316219  
GENERAL INFORMATION:  
APPLICANT: KRIEF, STEPHANE  
APPLICANT: SOUCHET, MICHEL  
APPLICANT: BRIL, ANTOINE  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GH-30985  
CURRENT APPLICATION NUMBER: US/09/160,119A  
CURRENT FILING DATE: 1998-09-24  
EARLIER APPLICATION NUMBER: EP 97402511.6  
EARLIER FILING DATE: 1997-10-23  
EARLIER APPLICATION NUMBER: EP 98401655.0  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 674  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-09-160-119-2

QY 12 FLAGVAAAIKSTAVAPIERVELLQVQHASKQITADKQYKIIDCVRIKPEQEVLSFW 71  
DB 331 FGLSVAGVAGTAVYPIDLVKTRMONGRSTGSPVGEIMYKNSPDCFKVLRYEGFGLY 390  
QY 72 RGNLANVIRYPTQALNFAFKQKQIFL---GGVDKRTQFRRYAGNLASGAGAGATSL 128  
DB 391 RGLLPOLLGVAPEKAIKLTVDVFRDKFMHKGVSVP-----LAAEIIAGGCGAGGSQV 442  
QY 129 CFVYPLDPAFRLADVKGAGAREFRGLDCLVYIKYSDGKGLYOGFNVSVQGI 188  
DB 443 IFPMLELVKIRLQV-----AGEITTPRVSALSVRDGLFPGIYKAKACFLRDI 496  
QY 189 AAYFGIYDTAKGMLDPPKXTHIVISWMLAQVTAVAGLTS---YFPDTRRMMSQGR 244  
DB 497 AIVFCYAHVYKASPNEDQVSPGSLILA---GALAGMPASLVTPADVIKTR--LQVAA 551  
QY 245 KGTIMTGTLDCKRKIADDEGKAFPKGAMSVNLRMGG-AFVLVLYDEIKKY 297  
DB 552 RAGQTTYSVIDCPRKILREBGPALMKGAGARVRSSPQGVTLTYELLQRW 605

Query Match 16.9%; Score 261.5; DB 4; Length 674;  
Best Local Similarity 26.2%; Pred. No. 4.4e-21;  
Matches 77; Conservative 51; Mismatches 139; Indels 27; Gaps 7;

QY 12 FLAGVAAAIKSTAVAPIERVELLQVQHASKQITADKQYKIIDCVRIKPEQEVLSFW 71  
DB 331 FGLSVAGVAGTAVYPIDLVKTRMONGRSTGSPVGEIMYKNSPDCFKVLRYEGFGLY 390  
QY 72 RGNLANVIRYPTQALNFAFKQKQIFL---GGVDKRTQFRRYAGNLASGAGAGATSL 128  
DB 391 RGLLPOLLGVAPEKAIKLTVDVFRDKFMHKGVSVP-----LAAEIIAGGCGAGGSQV 442  
QY 129 CFVYPLDPAFRLADVKGAGAREFRGLDCLVYIKYSDGKGLYOGFNVSVQGI 188  
DB 443 IFPMLELVKIRLQV-----AGEITTPRVSALSVRDGLFPGIYKAKACFLRDI 496  
QY 189 AAYFGIYDTAKGMLDPPKXTHIVISWMLAQVTAVAGLTS---YFPDTRRMMSQGR 244  
DB 497 AIVFCYAHVYKASPNEDQVSPGSLILA---GALAGMPASLVTPADVIKTR--LQVAA 551  
QY 245 KGTIMTGTLDCKRKIADDEGKAFPKGAMSVNLRMGG-AFVLVLYDEIKKY 297  
DB 552 RAGQTTYSVIDCPRKILREBGPALMKGAGARVRSSPQGVTLTYELLQRW 605

RESULT 12  
US-09-142-565-2  
Sequence 2, Application US/09142565A  
Patent No. 6187560  
GENERAL INFORMATION:  
APPLICANT: Lee James Beeley  
APPLICANT: Kelly Paine  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GH-30002  
CURRENT APPLICATION NUMBER: US/09/142,565A  
CURRENT FILING DATE: 1999-06-30  
EARLIER APPLICATION NUMBER: 9704551.2  
EARLIER FILING DATE: 1997-03-05  
EARLIER APPLICATION NUMBER: 9705614.7  
EARLIER FILING DATE: 1997-03-18  
EARLIER APPLICATION NUMBER: 97305305.1  
EARLIER FILING DATE: 1997-07-16  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2  
LENGTH: 312  
TYPE: PRT  
ORGANISM: HOMO SAPIEN  
US-09-142-565-2

Query Match 16.0%; Score 247; DB 3; Length 312;  
Best Local Similarity 24.8%; Pred. No. 6, 2e-20;  
Matches 76; Conservative 56; Mismatches 149; Indels 26; Gaps 8;

QY 2 TDALSPADFLAGVAIAISTAVAPIERVLLIQVHASKQITADK--QYKGIIDCV 59  
DB 7 SDVPMTAVKFLGATACFADLTVPDLTAKVRLIQENQAVQTARLVQRYGLTIL 66  
QY 60 RIRKQEVLSFKRNLAVIRFPQALNFAKDKTKKQIFL--GVDKKTQFRYAGNLA 118  
DB 67 TMVRTEGSPGPNGLVAGIQRMSPASIRIGLYDVKQVYTPKGDNSLTLTILA---- 122  
QY 119 SGAGATSLCFVYPLDFAFRLADV--GKAGAREPFGDCLVKIKSPDKIGLYOG 176  
DB 123 -GCTTGAAVTCQPTDVKVAFQASIHGSPSRDKISGTMADAYRTIAREGVGLMKG 181  
QY 177 FNVSVGGIIYRAAFGLYDIAK-----GMLDPPKATHIVISWMLAQTVTAAGLTSP 230  
DB 182 TLPNIMRNALVNCARVVTYDILKEKILDYHLLTDNPPCHFGVAFGAFCAIVVAS----P 237  
QY 231 PPTVRRMMQSGRGTDMITGTLDCWKRIARDGGAFFKGMANSVLR--GMGAPVLV 289  
DB 238 VDVTTRVY-----NSPPQYSPPLDCMKVVAQSGPTAFYKGTPTSPFLQSGMNVMFV 292  
QY 290 LYDEIKK 296  
DB 293 TYEQIAKR 299

## RESULT 13

US-08-775-009-33  
Sequence 33, Application US/08775009  
Patent No. 5935783

GENERAL INFORMATION:  
APPLICANT: Gong, Wellong  
APPLICANT: Emanuel, Beverly S.  
APPLICANT: Budarf, Marcia L.  
APPLICANT: Roe, Bruce  
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestion and  
TITLE OF INVENTION: Vellocardiofacial Syndrome Minimal Critical Region  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz &  
ADDRESSER: No. 5935783is, LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/775,009  
FILING DATE: 27-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Trujillo, Doreen Yalko  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CH-0681  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3439  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:

LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-775-009-33

Query Match 15.8%; Score 244.5; DB 2; Length 311;  
Best Local Similarity 28.1%; Pred. No. 1, 2e-19;  
Matches 83; Conservative 47; Mismatches 138; Indels 27; Gaps 8;

QY 10 KDPLAGVAAIAISTAVAPIERVLLIQVHASKQITADKQYKGIIDCVIRPEQEVLS 69  
DB 27 KAILAGLAGIIEICITFEYVTKQQLDERRAN-----PPRIKIGDVRQYVSHGLG 82  
QY 70 FWRGNLAVIRFPQALNFA--PKQYKQIFLAGVDKKTQFRYAGNLA SGAGAT 126  
DB 83 LYRGISILYGSIFRAAVRFQMFPEFLSNHMDAQGRIDSR-----RGLICGLAGVAB 135  
QY 127 SLCPVYPLDFAFRLADVAGAGAREPFGDCLVKIKSPDKIGLYOGFNVSVQGI 186  
DB 136 AVVVCPMEYVAKFIHD--QTSNPKYRGFFHGVREIVRQGLKGYQGLTATVLKQGS 193  
QY 187 YRAAFGLYDIAKGLDPPKATHIVISWMLAQTVTAAGLTSP-----PPTVRRMMQGS 242  
DB 194 NQAIRFPMTSLRWY--GQDNPNKPNPLINGVGAAGAASVGNTPLDVIKTRMGLB 252  
QY 243 GRKGTDMITGTLDCWKRIARDGGAFFKGMANSVLR--GMGAPVLVLYDEIKK 296  
DB 253 AHK-----YRNTLDGVOILKNEGPKAFYKGTVPRLGVCIDVAIVFYIDYEVAK 302

## RESULT 14

US-08-518-878B-51  
Sequence 51, Application US/08518878B  
Patent No. 5702302

GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/518,878B  
FILING DATE: 23-AUG-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-036  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
US-08-518-878B-51

Query Match 15.5%; Score 239.5; DB 1; Length 309;  
 Best Local Similarity 23.5%; Pred. No. 4.4e-19;  
 Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

2 TDAALSPADFLAGVAAAIKSTAVAPIERVKLLQVQHASK---QITADKQYKGIIDCV 58  
 7 TDVPTATVTKFLGAGTACIADLITFPLDTAKVRLQIGSESGPVRATVSAQYGVMGTI 66  
 59 VRIPEQEVLSFWRGNLANVIRFFTOALNFAFDKXQIPLGVDKRTQWRRYAGNLA 118  
 67 LTMVTEGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFTKSEHAS-----IGSRL 121  
 119 SGGAAGATSLCFVYPLDFARFLADVGAAGAREFRGLDCLVYIKYSDGIKGLYOGFN 178  
 122 AGSTTGALAVAAVQPTDVVKYRFQAO-ARAAGGRYOSTVNAKYTIAREBGRGLMKGTS 180  
 179 VSVGGIITRYRAYFGIYDTAK-----GMLPDPKNTHTIVISMTAQVTVAAGLTSYFPD 232  
 181 PNVARNAIVNCABELVYTDLIKDALIKANLMTDDLPCFTSAFGAGFCTTVIAS----PVD 236  
 233 TVRRRMNQOS-GRKGTDMYTGTLDCWRKIARDDEGKAFFGAGMSNVLR-GMGAFVLYL 290  
 237 VKTRRYNSALGQ-----YSSAGHCALTMLQKEGPRAFYKGFMPSPFLGSMNVVMFVT 290  
 291 YDEIKK 296  
 291 YEQLKR 296

RESULT 15  
 US-08-807-861A-51  
 ; Sequence 51, Application US/08807861A

GENERAL INFORMATION:  
 APPLICANT: Tartaglia, Louis A.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
 NUMBER OF SEQUENCES: 64  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/807,861A  
 FILING DATE: 26-FEB-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/518,878  
 FILING DATE: 23-AUG-1995  
 APPLICATION NUMBER: US 08/470,868  
 FILING DATE: 06-JUN-1995  
 APPLICATION NUMBER: US 08/294,522  
 FILING DATE: 23-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Corluzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7853-066  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 INFORMATION FOR SEQ ID NO: 51:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 309 amino acids  
 TYPE: amino acid

STRANDEDNESS: single  
 ;  
 ; TOPOLOGY: unknown  
 ;  
 US-08-807-861A-51

Query Match 15.5%; Score 239.5; DB 2; Length 309;  
 Best Local Similarity 23.5%; Pred. No. 4.4e-19;  
 Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

2 TDAALSPADFLAGVAAAIKSTAVAPIERVKLLQVQHASK---QITADKQYKGIIDCV 58  
 7 TDVPTATVTKFLGAGTACIADLITFPLDTAKVRLQIGSESGPVRATVSAQYGVMGTI 66  
 59 VRIPEQEVLSFWRGNLANVIRFFTOALNFAFDKXQIPLGVDKRTQWRRYAGNLA 118  
 67 LTMVTEGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFTKSEHAS-----IGSRL 121  
 119 SGGAAGATSLCFVYPLDFARFLADVGAAGAREFRGLDCLVYIKYSDGIKGLYOGFN 178  
 122 AGSTTGALAVAAVQPTDVVKYRFQAO-ARAAGGRYOSTVNAKYTIAREBGRGLMKGTS 180  
 179 VSVGGIITRYRAYFGIYDTAK-----GMLPDPKNTHTIVISMTAQVTVAAGLTSYFPD 232  
 181 PNVARNAIVNCABELVYTDLIKDALIKANLMTDDLPCFTSAFGAGFCTTVIAS----PVD 236  
 233 TVRRRMNQOS-GRKGTDMYTGTLDCWRKIARDDEGKAFFGAGMSNVLR-GMGAFVLYL 290  
 237 VKTRRYNSALGQ-----YSSAGHCALTMLQKEGPRAFYKGFMPSPFLGSMNVVMFVT 290  
 291 YDEIKK 296  
 291 YEQLKR 296

Search completed: December 18, 2003, 12:44:55  
 Job time : 13.3471 secs



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## OM protein - protein search, using sw model

Run on: December 18, 2003, 12:43:17 ; Search time 24.3606 Seconds

(without alignments)  
2284.595 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547  
Sequence: 1 MTDAALSPADFLAGVAA.....LRGNGAFVLVYDEIKKYT 298Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1547	100.0	298	9	US-09-811-094-32
2	1547	100.0	298	9	US-09-810-644-32
3	1547	100.0	298	10	US-09-185-904A-32
4	1454	94.0	298	9	US-09-811-094-33
5	1454	94.0	298	9	US-09-810-644-33
6	1454	94.0	298	10	US-09-185-904A-33
7	1391.5	89.9	297	9	US-09-811-094-31
8	1391.5	89.9	297	9	US-09-810-644-31
9	1391.5	89.9	297	10	US-09-185-904A-31
10	840	54.3	179	12	US-10-029-386-32501
11	779.5	50.4	301	12	US-10-032-585-7194
12	752.5	48.6	318	10	US-09-801-368-252
13	741.5	47.9	381	12	US-10-141-478A-2
14	741.5	47.9	386	9	US-09-734-559-170
15	734	47.4	308	15	US-10-128-714-3338

16	734	47.4	308	15	US-10-128-714-8338	Sequence 8338, Ap
17	677.5	43.8	677	12	US-10-259-165-192	Sequence 192, Ap
18	484	31.3	132	9	US-09-925-301-1459	Sequence 1459, Ap
19	448	29.0	87	9	US-09-864-761-36440	Sequence 36440, A
20	351	22.7	477	10	US-09-777-921A-2	Sequence 2, Appl1
21	350	22.6	475	10	US-09-777-921A-4	Sequence 4, Appl1
22	323.5	20.9	410	10	US-09-777-921A-5	Sequence 5, Appl1
23	309	20.0	384	12	US-10-094-749-1789	Sequence 1789, Ap
24	302	19.5	469	9	US-09-989-722-289	Sequence 289, Ap
25	302	19.5	469	9	US-09-989-723-289	Sequence 289, Ap
26	302	19.5	469	9	US-09-989-279-289	Sequence 289, Ap
27	302	19.5	469	9	US-09-989-727-289	Sequence 289, Ap
28	302	19.5	469	10	US-09-989-732-289	Sequence 289, Ap
29	302	19.5	469	10	US-09-991-073-289	Sequence 289, Ap
30	302	19.5	469	10	US-09-991-442-289	Sequence 289, Ap
31	302	19.5	469	10	US-09-991-163-289	Sequence 289, Ap
32	302	19.5	469	10	US-09-993-604-289	Sequence 289, Ap
33	302	19.5	469	10	US-09-990-444-289	Sequence 289, Ap
34	302	19.5	469	10	US-09-989-721-289	Sequence 289, Ap
35	302	19.5	469	10	US-09-992-598-289	Sequence 289, Ap
36	302	19.5	469	10	US-09-989-735-289	Sequence 289, Ap
37	302	19.5	469	10	US-09-989-735-289	Sequence 289, Ap
38	302	19.5	469	10	US-09-990-444-289	Sequence 289, Ap
39	302	19.5	469	10	US-09-991-181-289	Sequence 289, Ap
40	302	19.5	469	10	US-09-989-730-289	Sequence 289, Ap
41	302	19.5	469	10	US-09-990-436-289	Sequence 289, Ap
42	302	19.5	469	10	US-09-993-687-289	Sequence 289, Ap
43	302	19.5	469	11	US-09-989-734-289	Sequence 289, Ap
44	302	19.5	469	11	US-09-997-653-289	Sequence 289, Ap
45	302	19.5	469	11	US-09-997-653-289	Sequence 289, Ap

## ALIGNMENTS

RESULT 1  
US-09-811-094-32  
Sequence 32, Application US/09811094  
Patient No. US2001004144A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Willey, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D4  
CURRENT APPLICATION NUMBER: US/09/811,094  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-811-094-32  
Query Match 100.0%; Score 1547; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 6.6e-159;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MTDAALSPADFLAGVAAISKRAVPIRKYLLLOVQASAKQITADKYKGIIDCVR 60  
DB 1 MTDAALSPADFLAGVAAISKRAVPIRKYLLLOVQASAKQITADKYKGIIDCVR 60  
OY 1PKQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFGSGVDKRTQFRYPAGNLAAG 120  
DB 1PKQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFGSGVDKRTQFRYPAGNLAAG 120

QY 121 GAAGATSICTFYPLDPARTRLAADVKGAGAEERFGLDCLVKIKYSDIGIKLYOGFNV 180  
DB 121 GAAGATSICTFYPLDPARTRLAADVKGAGAEERFGLDCLVKIKYSDIGIKLYOGFNV 180  
QY 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSPDTPVRRMM 240  
DB 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSPDTPVRRMM 240  
QY 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGMGAFVLVLYDEIKKYT 298  
DB 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGMGAFVLVLYDEIKKYT 298

RESULT 2  
US-09-810-644-32  
; Sequence 32, Application US/09810644  
; Patent No. US20020012992A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Cleveenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Miller, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Moos, Walter H.  
; APPLICANT: Pel, Yazhong  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
; FILE REFERENCE: 660088.420D3  
; CURRENT APPLICATION NUMBER: US/09/810,644  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-810-644-32

Query Match 100.0%; Score 1547; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 6.6e-159;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCYVR 60  
DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCYVR 60  
QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
DB 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
QY 121 GAAGTSTICTFYPLDPARTRLAADVKGAGAEERFGLDCLVKIKYSDIGIKLYOGFNV 180  
DB 121 GAAGTSTICTFYPLDPARTRLAADVKGAGAEERFGLDCLVKIKYSDIGIKLYOGFNV 180  
QY 121 GAAGTSTICTFYPLDPARTRLAADVKGAGAEERFGLDCLVKIKYSDIGIKLYOGFNV 180  
DB 121 GAAGTSTICTFYPLDPARTRLAADVKGAGAEERFGLDCLVKIKYSDIGIKLYOGFNV 180  
QY 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSPDTPVRRMM 240  
DB 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSPDTPVRRMM 240  
QY 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGMGAFVLVLYDEIKKYT 298  
DB 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGMGAFVLVLYDEIKKYT 298

RESULT 3  
US-09-185-904A-32  
; Sequence 32, Application US/09185904A  
; Patent No. US2002017185A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.

APPLICANT: Cleveenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Miller, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
; FILE REFERENCE: 660088.420  
; CURRENT APPLICATION NUMBER: US/09/185,904A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-185-904A-32

Query Match 100.0%; Score 1547; DB 10; Length 298;  
Best Local Similarity 100.0%; Pred. No. 6.6e-159;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCYVR 60  
DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCYVR 60  
QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
DB 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
QY 121 GAAGTSTICTFYPLDPARTRLAADVKGAGAEERFGLDCLVKIKYSDIGIKLYOGFNV 180  
DB 121 GAAGTSTICTFYPLDPARTRLAADVKGAGAEERFGLDCLVKIKYSDIGIKLYOGFNV 180  
QY 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSPDTPVRRMM 240  
DB 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSPDTPVRRMM 240  
QY 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGMGAFVLVLYDEIKKYT 298  
DB 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGMGAFVLVLYDEIKKYT 298

RESULT 4  
US-09-811-094-33  
; Sequence 33, Application US/09811094  
; Patent No. US2001004414A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Cleveenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Miller, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Moos, Walter H.  
; APPLICANT: Pel, Yazhong  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
; FILE REFERENCE: 660088.420D4  
; CURRENT APPLICATION NUMBER: US/09/811,094  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-811-094-33

Query Match 94.0%; Score 1454; DB 9; Length 298;  
Best Local Similarity 92.6%; Pred. No. 7.7e-149;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy	1	MTAAALSFPADFLAAGVAAAI	SKTAAV	PERKLLQVQHASK	OTADKQVGIIDCVR	60
		1	1	1	1	
Db	1	MTGQALSPADFLAAGIAAAI	SKTAAV	PERKLLQVQHASK	OTADKQVGIIDCVR	60
Qy	120	1PKQEVLSFWRGNTLANVIR	YFPTQALNFAFDKKQI	FLGVDKRTQFWRYFAGNTASG	120	
		61	1	1	1	
Db	120	1PKQGVLSFWRGNTLANVIR	YFPTQALNFAFDKKQI	FLGVDKRTQFWRYFAGNTASG	120	
		61	1	1	1	
Qy	121	GAAGATSLCVVYGLDFAFRT	LIADVCKAAEEFPGLD	CIWKLYKSGIKGLVQGENVS	180	
		121	1	1	1	
Db	121	GAAGATSLCVVYGLDFAFRT	LIADVCKAAEEFPGLD	CIWKLYKSGIKGLVQGENVS	180	
		121	1	1	1	
Qy	181	VGGIIIVRAAYFSGIYDTAG	MLPDPKNTHTIVISMM	IAQTVAIVAGLTSYSPDYTRRRMM	240	
		181	1	1	1	
Db	181	VGGIIIVRAAYFSGIYDTAG	MLPDPKNTHTIVISMM	IAQTVAIVAGVSYSPDYTRRRMM	240	
		181	1	1	1	
Qy	241	QSGRKGDIMYTGTLQCMRK	LIARDEBGRKFFFGAASNT	LRMGGAFLVLYLDELTK	296	
		241	1	1	1	
Db	241	QSGRKGDIMYTGTLQCMRK	LIARDEBGRKFFFGAASNT	LRMGGAFLVLYLDELTK	296	
		241	1	1	1	

RESULT 5  
US-09-810-644-33

```

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert R.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Kileen
APPLICANT: Wiley, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660068.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PR1
ORGANISM: Homo sapien
OS-09-810-644-33

```

Query Match	94.0%;	Score 1454;	DB 9;	Length 298;
Best Local Similarity	92.6%;	Pred. No. 7.7e-149;		
Matches 274;	Conservative 13;	Mismatches 9;	Indels 0;	Gaps 0;

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QY      1  MTPAALSPADPFLAGVAALAIKTAAPERIKVLLQVQHASKOITADKQYKGIIDCVR  60
Dh      1  MEGQALSPAKDPLAGGIAAISKANAPERIKVLLQVQHASKOITADKQYKGIIDCVR  60
QY      61  ITPKQRYVLSFWRGNLANVIRYPTQALNFAFKDKTKQIFLGQVDRKQFWMYRPAAGIASG  120
Dh      61  ITPKQRYVLSFWRGNLANVIRYPTQALNFAFKDKTKQIFLGQVDRKQFWMYRPAAGIASG  120
QY      121  GAAGATSLCVVPPLDPAFTRTLAADQKGAEREFGGLDCLVKIKYKDGKIKGLYQGFNV  180
Dh      121  GAAGATSLCVVPPLDPAFTRTLAADQKGSTEREFGGLDCLVKIKYKDGKIKGLYQGFNV  180
QY      181  VQGIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMAQTVTAVAAGLTSTYEDTVRRMM  240
Dh      181  VQGIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMAQTVTAVAAGVNSPYDTVRRMM  240
QY      241  QSRKQKGDIMTGTLLDMRKIARDBEGKRFEGGAASNLBGMGAFVLVLYDEIKK  296
Dh      241  QSRKQKADIMTGTVDMCRKIFRDBEGKRFEGGAASNLBGMGAFVLVLYDEIKK  296

```

RESULT 6  
US-09-185-904A-33

```

1  APPLICANT: Anderson, Christen M.
2  APPLICANT: Davis, Robert E.
3  APPLICANT: Clevenger, William
4  APPLICANT: Wiley, Sandra Eileen
5  APPLICANT: Willey, Scott W.
6  APPLICANT: Szabo, Tomas R.
7  APPLICANT: Ghosh, Soumitra S.
8  TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
9  TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
10 TITLE OF INVENTION: THEREFOR
11 FILE REFERENCE: 660088.420
12 CURRENT APPLICATION NUMBER: US/09/185,904A
13 CURRENT FILING DATE: 1998-11-03
14 NUMBER OF SEQ ID NOS: 33
15 SOFTWARE: FastSeq for Windows Version 3.0
16 SEQ ID NO: 33
17 LENGTH: 298
18 TYPE: PRM
19 ORGANISM: Homo sapien
20 US-09-185-904A-33

```

Query Match	94.0%;	Score 1454;	DB 10;	Length 298;
Best Local Similarity	92.6%;	Pred. NO. 7.7e-149;		
Matches 274;	Conservative 13;	Mismatches 9;	Indels 0;	Gaps 0;

Qy	1	MDPAASP	KD	LAGV	AA	SKTA	VA	IE	EV	LL	QV	HA	SK	IT	AD	KY	IG	CV	60																														
			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:																															
Db	1	MEQ	AS	SP	KD	LAG	IA	AA	SK	TA	VA	IE	EV	KL	LL	QV	HA	SK	IT	AD	KY	IG	CV	60																									
Qy	61	IP	KR	EV	LS	PM	R	GN	L	A	N	I	R	Y	E	P	T	O	A	N	F	A	K	D	K	K	O	I	P	L	G	V	D	K	R	T	O	W	R	F	A	G	N	I	A	S	G	120	
Db	61	IP	KR	EV	LS	PM	R	GN	L	A	N	I	R	Y	E	P	T	O	A	N	F	A	K	D	K	K	O	I	P	L	G	V	D	K	R	T	O	W	R	F	A	G	N	I	A	S	G	120	
Qy	121	GA	GA	NS	L	CF	NY	P	L	D	F	A	R	T	R	L	A	D	V	G	K	A	E	R	E	R	G	I	C	D	C	I	Y	K	E	S	D	G	I	K	G	I	Y	O	G	N	S	180	
Db	121	GA	GA	NS	L	CF	NY	P	L	D	F	A	R	T	R	L	A	D	V	G	K	A	E	R	E	R	G	I	C	D	C	I	Y	K	E	S	D	G	I	K	G	I	Y	O	G	N	S	180	
Qy	181	VO	G	I	I	I	R	A	A	E	G	I	D	T	A	K	M	L	P	D	K	N	H	I	A	I	S	M	M	I	A	Q	T	A	V	A	G	L	S	E	P	E	D	T	R	R	M	M	240
Db	181	VO	G	I	I	I	R	A	A	E	G	I	D	T	A	K	M	L	P	D	K	N	H	I	A	I	S	M	M	I	A	Q	T	A	V	A	G	L	S	E	P	E	D	T	R	R	M	M	240
Qy	241	Q	S	R	K	E	T	D	I	M	T	G	L	D	C	R	K	T	A	P	B	E	G	G	A	P	F	K	M	S	V	L	T	G	M	G	A	P	T	L	Y	D	E	I	K	296			
Db	241	Q	S	R	K	E	T	D	I	M	T	G	L	D	C	R	K	T	A	P	B	E	G	G	A	P	F	K	M	S	V	L	T	G	M	G	A	P	T	L	Y	D	E	I	K	296			
Qy	241	Q	S	R	K	E	T	D	I	M	T	G	L	D	C	R	K	T	A	P	B	E	G	G	A	P	F	K	M	S	V	L	T	G	M	G	A	P	T	L	Y	D	E	I	K	296			
Db	241	Q	S	R	K	E	T	D	I	M	T	G	L	D	C	R	K	T	A	P	B	E	G	G	A	P	F	K	M	S	V	L	T	G	M	G	A	P	T	L	Y	D	E	I	K	296			

RESULT 7  
US-09-811-094-31  
Sequence 31, Application US/09811094

APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Willey, Sandra Bileen  
APPLICANT: Willey, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pei, Yachong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.42004  
CURRENT APPLICATION NUMBER: US/09/811,094  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-811-094-31

Query Match 89.9%; Score 1391.5; DB 9; Length 297;  
 Best Local Similarity 88.6%; Pred. No. 4.5e-142;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
 DB 1 MGDHMSFLKDFLAGVAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRR 60  
 QY 61 IPKEQEVLSFWRGKLNANIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
 DB 61 IPKEGGLSFWRGNLANIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYVPDLPARTRLAADVKGAGAEERFGLDCLVKIYKSDGKGLYGFVNS 180  
 DB 121 GAAGATSLCFYVPDLPARTRLAADVGRR-AQREHFGLDCLIKIKPSDGLKGLYGFVNS 179  
 QY 181 VGGIITRAAYFGYDPAKGMPLDPKNTHTIVISNMIAQTVAAGLTSYPTVRRRRMM 240  
 DB 180 VGGIITRAAYFGYDPAKGMPLDPKNTHTIVISNMIAQSVTAAGLTSYPTVRRRRMM 239  
 QY 241 QSGRGTIDIMYTGTLDCWRKIARDDEGKAFPKGAMSNVLRGMGAFVLVYDEIKKY 297  
 DB 240 QSGRKGADIMYTGTVDCWRKIARDDEGAKAFPKGAMSNVLRGMGAFVLVYDEIKKY 296

## RESULT 8

US-09-810-644-31  
 Sequence 31, Application US/09810644  
 Patent No. US20020012992A1

GENERAL INFORMATION:  
 APPLICANT: Anderson, Christen M.  
 APPLICANT: Davis, Robert E.  
 APPLICANT: Cleveland, William  
 APPLICANT: Wiley, Sandra Eileen  
 APPLICANT: Szabo, Thomas R.  
 APPLICANT: Ghosh, Soumitra S.  
 APPLICANT: Moses, Walter H.  
 APPLICANT: Pei, Yashong  
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 FILE REFERENCE: 660088.420D3  
 CURRENT APPLICATION NUMBER: US/09/810,644  
 CURRENT FILING DATE: 2001-03-14  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-810-644-31

Query Match 89.9%; Score 1391.5; DB 9; Length 297;  
 Best Local Similarity 88.6%; Pred. No. 4.5e-142;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
 DB 1 MGDHMSFLKDFLAGVAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRR 60  
 QY 61 IPKEQEVLSFWRGKLNANIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
 DB 61 IPKEGGLSFWRGNLANIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYVPDLPARTRLAADVKGAGAEERFGLDCLVKIYKSDGKGLYGFVNS 180  
 DB 121 GAAGATSLCFYVPDLPARTRLAADVGRR-AQREHFGLDCLVKIYKSDGKGLYGFVNS 180

DB 121 GAAGATSLCFYVPDLPARTRLAADVGRR-AQREHFGLDCLIKIKPSDGLKGLYGFVNS 179  
 QY 181 VGGIITRAAYFGYDPAKGMPLDPKNTHTIVISNMIAQTVAAGLTSYPTVRRRRMM 240  
 DB 180 VGGIITRAAYFGYDPAKGMPLDPKNTHTIVISNMIAQSVTAAGLTSYPTVRRRRMM 239  
 QY 241 QSGRGTIDIMYTGTLDCWRKIARDDEGKAFPKGAMSNVLRGMGAFVLVYDEIKKY 297  
 DB 240 QSGRKGADIMYTGTVDCWRKIARDDEGAKAFPKGAMSNVLRGMGAFVLVYDEIKKY 296

## RESULT 9

US-09-185-904A-31  
 Sequence 31, Application US/09185904A  
 Patent No. US20020177185A1

GENERAL INFORMATION:  
 APPLICANT: Anderson, Christen M.  
 APPLICANT: Davis, Robert E.  
 APPLICANT: Cleveland, William  
 APPLICANT: Wiley, Sandra Eileen  
 APPLICANT: Szabo, Thomas R.  
 APPLICANT: Ghosh, Soumitra S.  
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
 TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
 TITLE OF INVENTION: THEREFOR  
 FILE REFERENCE: 660088.420  
 CURRENT APPLICATION NUMBER: US/09/185,904A  
 CURRENT FILING DATE: 1998-11-03  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-185-904A-31

Query Match 89.9%; Score 1391.5; DB 10; Length 297;  
 Best Local Similarity 88.6%; Pred. No. 4.5e-142;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
 DB 1 MGDHMSFLKDFLAGVAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRR 60  
 QY 61 IPKEQEVLSFWRGKLNANIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
 DB 61 IPKEGGLSFWRGNLANIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYVPDLPARTRLAADVKGAGAEERFGLDCLVKIYKSDGKGLYGFVNS 180  
 DB 121 GAAGATSLCFYVPDLPARTRLAADVGRR-AQREHFGLDCLIKIKPSDGLKGLYGFVNS 179  
 QY 181 VGGIITRAAYFGYDPAKGMPLDPKNTHTIVISNMIAQTVAAGLTSYPTVRRRRMM 240  
 DB 180 VGGIITRAAYFGYDPAKGMPLDPKNTHTIVISNMIAQSVTAAGLTSYPTVRRRRMM 239  
 QY 241 QSGRGTIDIMYTGTLDCWRKIARDDEGKAFPKGAMSNVLRGMGAFVLVYDEIKKY 297  
 DB 240 QSGRKGADIMYTGTVDCWRKIARDDEGAKAFPKGAMSNVLRGMGAFVLVYDEIKKY 296

## RESULT 10

US-10-029-386-32501  
 Sequence 32501, Application US/10029386  
 Publication No. US20030194704A1

GENERAL INFORMATION:  
 APPLICANT: Penn, Sharron G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
 TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
 FILE REFERENCE: A60MICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 32501  
LENGTH: 179  
TYPE: PR1  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC004000.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96  
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU2 2.00e-83  
US-10-029-386-32501

Query Match 54.3%; Score 840; DB 12; Length 179;  
Best Local Similarity 98.8%; Pred. No. 1,1e-82;  
Matches 161; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 VQHASKQITADKQYKGIIDCVRIPEQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQ 97  
DB 1 VQHASKQITADKQYKGIIDCVRIPEQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQ 60

QY 98 IFPGVDKRTQPMYRPAAGNLASGGAAGTSLCFYVPLDPATRLAADVKGABERFGL 157  
DB 61 IFPGVDKRTQPMYRPAAGNLASGGAAGTSLCFYVPLDPATRLAADVKGABERFGL 120

QY 158 GDCLVKIYKSDIKGLYOGFNVSVGGIITRYAAYGIVDTAKG 200  
DB 121 GDCLVKIYKSDIKGLYOGFNVSVGGIITRYAAYGIVDTAKG 163

RESULT 11  
US-10-032-585-7194  
Sequence 7194, Application US/10032585  
Publication No. US20030180953A1  
GENERAL INFORMATION:  
APPLICANT: Terry, Roemer D.  
APPLICANT: Bo, Jiang  
APPLICANT: Charles, Boone  
APPLICANT: Howard, Bussey  
TITLE OR INVENTION: Gene Disruption Methodologies for Drug Target Discovery  
FILE REFERENCE: 10182-005-999  
CURRENT APPLICATION NUMBER: US/10/032,585  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 8000  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7194  
LENGTH: 301  
TYPE: PR1  
ORGANISM: Candida albicans  
US-10-032-585-7194

Query Match 50.4%; Score 779.5; DB 12; Length 301;  
Best Local Similarity 54.5%; Pred. No. 8e-76;  
Matches 163; Conservative 41; Mismatches 84; Indels 11; Gaps 6;

QY 1 MTDALSAKDFLAGVAAATSKTAVAPIERVKLLIQVQ-HASKQITADKQYKGIIDCV 59  
DB 1 MTDALSAKDFLAGVAAATSKTAVAPIERVKLLIQVQ-HASKQITADKQYKGIIDCV 58

QY 60 RIPKQEVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKRTQPMYRPAAGNLAS 119  
DB 59 RTADEGVSVFMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKRTQPMYRPAAGNLAS 116

QY 120 GGAAGATSLCFYVPLDPATRLAADV--GKAGABERFGLGDCLVKIYKSDIKGLYOGF 177  
DB 117 GGLAGATSLAFYVPLDPATRLAADV--GKAGABERFGLGDCLVKIYKSDIKGLYOGF 176

QY 178 NVSVGGIITRYAAYGIVDTAKG-MLPDPKTHIVISMMIAQTVTAAGLISYPPDVTNR 236

DB 177 GPVSIGIVVIRGLYFGIYDLSKPVVLYGPLEGSLAFILGMAVTTGASTASYPLDVTNR 236

QY 237 RMMQSGRKGTDMVTGTLDCWKRIADBGKAPFKGAMSIVLRGMGAFVLYVDEIK 295  
DB 237 RMMQSGRKGTDMVTGTLDCWKRIADBGKAPFKGAMSIVLRGMGAFVLYVDEIK 292

RESULT 12  
US-09-801-368-252  
Sequence 252, Application US/09801368  
Patent No. US20020128250A1  
GENERAL INFORMATION:  
APPLICANT: Bueby, Robert  
APPLICANT: Call, Brian  
APPLICANT: Hecht, Peter  
APPLICANT: Holtzman, Doug  
APPLICANT: Madden, Kevin  
APPLICANT: Maxon, Mary  
APPLICANT: Milne, Todd  
APPLICANT: No. US20020128250A1man, Thea  
APPLICANT: Royer, John  
APPLICANT: Salama, Sofie  
APPLICANT: Sherman, Amir  
APPLICANT: Silva, Jeff  
APPLICANT: Summers, Eric  
TITLE OR INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
FILE REFERENCE: 109272.147  
CURRENT APPLICATION NUMBER: US/09/801,368  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 09/487,558  
PRIOR FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: US 60/160,587  
PRIOR FILING DATE: 1999-10-20  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 252  
LENGTH: 318  
TYPE: PR1  
ORGANISM: Saccharomyces cerevisiae  
US-09-801-368-252

Query Match 48.6%; Score 752.5; DB 10; Length 318;  
Best Local Similarity 54.3%; Pred. No. 7.2e-73;  
Matches 159; Conservative 40; Mismatches 85; Indels 9; Gaps 5;

QY 7 SFAPDFLAGVAAATSKTAVAPIERVKLLIQVQ-HASKQITADKQYKGIIDCVRIPEQ 65  
DB 22 NFLIDFLMGVSAVAATKASPIERVKLLIQVQ-HASKQITADKQYKGIIDCVRIPEQ 81

QY 66 EVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKRTQPMYRPAAGNLASGAGA 125  
DB 82 EVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKRTQPMYRPAAGNLASGAGA 139

QY 126 TSLCFYVPLDPATRLAAD--VGKABERFGLGDCLVKIYKSDIKGLYOGFNVSV 183  
DB 140 TSLCFYVPLDPATRLAAD--VGKABERFGLGDCLVKIYKSDIKGLYOGFNVSV 199

QY 184 IIVRYAAYGIVDTAKG-MLPDPKTHIVISMMIAQTVTAAGLISYPPDVTNRMMQ 242  
DB 200 IIVRYAAYGIVDTAKG-MLPDPKTHIVISMMIAQTVTAAGLISYPPDVTNRMMQ 259

QY 243 GRKGTDMVTGTLDCWKRIADBGKAPFKGAMSIVLRGMGAFVLYVDEIK 295  
DB 260 GRKGTDMVTGTLDCWKRIADBGKAPFKGAMSIVLRGMGAFVLYVDEIK 309

RESULT 13  
US-10-141-478A-2  
Sequence 2, Application US/10141478A  
Publication No. US20030148300A1  
GENERAL INFORMATION:  
APPLICANT: Valentín, Henry

APPLICANT: Savage, Thomas  
APPLICANT: Voelker, Toni  
APPLICANT: Zang, Wei  
TITLE OF INVENTION: Metabolite Transporters  
FILE REFERENCE: 16515.146  
CURRENT APPLICATION NUMBER: US/10/141,478A  
CURRENT FILING DATE: 2002-05-09  
PRIOR APPLICATION NUMBER: US 60/289,519  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: 60/289,527  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 16517.  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 381  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-141-478A-2

Query Match 47.9%; Score 741.5; DB 12; Length 381;  
Best Local Similarity 53.6%; Pred. No. 1.4e-71;  
Matches 165; Conservative 38; Mismatches 78; Indels 27; Gaps 8;

QY 7 SPADFLAGVAAAIKSTAVAPIERVKLLQVQHASQOITA--DKQYKGIIDCVVRIPK 63  
DB NFALDFPLMGVSAVSKTAAAPIERVKLLIQNQ--DEMIIKAGRLSEPYKIGIDCFGRITK 136  
QY 64 EGVLSFPMGNLANVIRYPTQALNPAFDKQKQIFLGVDKRTQFMRYPPAGNLASGAA 123  
DB 137 DEGFSLRGNTANVIRYPTQALNPAFDKQKQIFLGVDKRTQFMRYPPAGNLASGAA 195  
QY 124 GATSLCFVYPLDPARTLAADV---GKAGABERFRGLGDCLVKIKYSDGIKGLYQGFNV 180  
DB 196 GASLFLFYSLDYARTRILANDAKSKKGGGQFNGLVYKKTATDGIAGLYRGPATSCA 255  
QY 181 VGGIIRYAAIFGIYDTAK---GMLDPKNTIIVISMIAGTVTAAGLTSPYPTVR 235  
DB 256 CVGIIVYGLVYGLDYSPVLLTGDLQSPFASPALGVI---TNGAGLASYPIDTVR 311  
QY 226 RRMWQSGRKGDIMYTGTLDCWKRIARDEGKAPFKGAMSVNLRGMAFVLYYDEI- 294  
DB 312 RRMWTSNEA---VKYKSLDAFKQILNKGAKSLFKAGANILRAVAGVLSGYDKLT 368  
QY 295 -----KKY 297  
DB 369 LIVRGKCY 376

RESULT 14  
US-09-734-569-170  
Sequence 170, Application US/09734569  
Patent No. US20020064816A1  
GENERAL INFORMATION:  
APPLICANT: Lersch, Jens  
APPLICANT: Renz, Andreas  
APPLICANT: Ehrhardt, Thomas  
APPLICANT: Reindl, Andreas  
APPLICANT: Clupus, Petra  
APPLICANT: Bleschhoff, Friedrich  
APPLICANT: Frank, Markus  
APPLICANT: Freund, Annette  
APPLICANT: Duwendig, Elke  
APPLICANT: Schmidt, Ralf-Michael  
APPLICANT: Reekti, Ralf

TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved  
in the synthesis of carbohydrates  
FILE REFERENCE: BASP-NAE-1332-99-US  
CURRENT APPLICATION NUMBER: US/09/734,569  
CURRENT FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 60/171,101  
PRIOR FILING DATE: 1999-12-16

NUMBER OF SEQ ID NOS: 181  
SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1  
SEQ ID NO 170  
LENGTH: 386  
TYPE: PRT  
ORGANISM: Physcomitrella patens  
US-09-734-569-170

Query Match 47.9%; Score 741.5; DB 9; Length 386;  
Best Local Similarity 53.4%; Pred. No. 1.5e-71;  
Matches 157; Conservative 42; Mismatches 86; Indels 9; Gaps 5;

QY 7 SPADFLAGVAAAIKSTAVAPIERVKLLQVQHASQOITA--DKQYKGIIDCVVRIPK 65  
DB 84 SFMTDFPLMGVSAVSKTAAAPIERVKLLIQNDEMISKGLSHPYKIGIDCFGRITVDE 143  
QY 66 EVLSPMGNLANVIRYPTQALNPAFDKQKQIFLGVDKRTQFMRYPPAGNLASGAA 125  
DB 144 GMSLPMRGNLANVIRYPTQALNPAFDKQKQIFLGVDKRTQFMRYPPAGNLASGAA 202  
QY 126 TSLCFVYPLDPARTLAADV---GKAGABERFRGLGDCLVKIKYSDGIKGLYQGFNV 182  
DB 203 SSLFLFYSLDYARTRILANDAKSKKGGGQFNGLVYKKTATDGIAGLYRGPATSCA 262  
QY 183 GIIRYAAIFGIYDTAK--MLPDKNTIIVISMIAGTVTAAGLTSPYPTVR 241  
DB 263 GIIVYGLVYGLDYSPVLLTGDLQSPFASPALGVI---TNGAGLASYPIDTVR 311  
QY 242 SGRKGTIDMYTGTLDCWKRIARDEGKAPFKGAMSVNLRGMAFVLYYDEI 295  
DB 323 SGEA---VKYKSLDAFKQILNKGAKSLFKAGANILRAVAGVLSGYDKLT 373

RESULT 15  
US-10-128-714-3338  
Sequence 3338, Application US/10128714  
Publication No. US20030119013A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Bo  
APPLICANT: Hu, Wenqi  
APPLICANT: Liabkoff, Daniel  
APPLICANT: Zamudio, Carlos  
APPLICANT: Eroskhin, Alexey M  
APPLICANT: Lemieux, Sebastien M  
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
Methods of Use  
FILE REFERENCE: 10182-018-999  
CURRENT APPLICATION NUMBER: US/10/128,714  
CURRENT FILING DATE: 2002-04-23  
PRIOR APPLICATION NUMBER: US 60/285,697  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: US 60/287,066  
PRIOR FILING DATE: 2001-04-27  
PRIOR APPLICATION NUMBER: US 60/295,890  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/303,899  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/316,362  
PRIOR FILING DATE: 2001-08-31  
NUMBER OF SEQ ID NOS: 8603  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3338  
LENGTH: 308  
TYPE: PRT  
ORGANISM: Aspergillus fumigatus  
US-10-128-714-3338

Query Match 47.4%; Score 734; DB 15; Length 308;  
Best Local Similarity 53.2%; Pred. No. 6.9e-71;  
Matches 157; Conservative 41; Mismatches 85; Indels 12; Gaps 6;

QY 7 SPADFLAGVAAAIKSTAVAPIERVKLLQVQHASQOITA--DKQYKGIIDCVVRIPK 63  
DB 157 DEGFSLRGNTANVIRYPTQALNPAFDKQKQIFLGVDKRTQFMRYPPAGNLASGAA 195

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Db      7 AFTDSFVAGVGSAAVSKTAAAPIERIKLL--VQNDQEMIRAGRLDPKKNKNIIDCFRRTAQ 64
Qy      64 EOEVLSPFRGNLANVIRIYPPQALNANFAFDKTKYQITPLGGVDKGTQWRIRFAGNLASGGAA 123
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65 AEGVSLWNGMGNANVIRYPPQALNANFAFDYKSMFAYKKD--RDGAKAMMGNILASGGAA 123
Qy      124 GATSLCPYVPLDPAFTRLADAV--GGAAGABREBERFGADCLVKIKSDGIKGLYQGFNVSV 181
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      124 GATSLLPFYSLDYARIRRLANDAKSANGGGRQNGLIDYVRKTLASDGLIYRGFQPSV 183
Qy      182 OGIIITYRAAYFEGIYDTAKG-MLPDPKQTHI VISMWTAQTYTAVAGLTSIPDFTVRRRRMM 240
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      184 LGIVVYRGILYFQMYSIKFVVLVGSLEGSFLASFLGFWLTVTGAAGIASYELDIPIRRRRMM 243
Qy      241 OSGRKGTIDMYGTGLDQWKRILADEGGKAFPKGAMSNVLRGMGAAPLVIYDETIK 295
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      244 TSGEA---VKYSSSLDAAQIILAKGYSKSLFKGAGNANIRGVAGAGVLTIDYDQV 295

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Search completed: December 18, 2003, 12:55:43  
Job time : 24.3606 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:40:52 ; Search time 165.852 Seconds  
(without alignments)  
1634.924 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547  
Sequence: 1 MTDALSPAKDFLAGVAA.....LRGNGAFVLYVDEIKYT 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:\*

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2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep:\*  
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30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep:\*  
31: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep:\*  
32: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	1	PCT-US01-15416-32

2	1547	100.0	298	15	US-09-185-904A-32	Sequence 32, Appl
3	1547	100.0	298	17	US-09-393-441-32	Sequence 32, Appl
4	1547	100.0	298	21	US-09-709-785-48	Sequence 48, Appl
5	1547	100.0	298	23	US-09-809-827-32	Sequence 32, Appl
6	1547	100.0	298	23	US-09-809-889-32	Sequence 32, Appl
7	1547	100.0	298	23	US-09-810-644-32	Sequence 32, Appl
8	1547	100.0	298	23	US-09-811-094-32	Sequence 32, Appl
9	1547	100.0	298	23	US-09-811-132-32	Sequence 32, Appl
10	1537	99.4	298	1	PCT-US02-01048-54	Sequence 54, Appl
11	1537	99.4	298	19	US-09-569-327-5	Sequence 5, Appl
12	1537	99.4	298	19	US-10-466-162-54	Sequence 54, Appl
13	1537	99.4	298	32	US-09-452-680-20286	Sequence 20286, A
14	1537	99.4	332	22	US-09-760-469-1767	Sequence 1767, Ap
15	1537	99.4	332	28	US-10-216-583-1767	Sequence 1767, Ap
16	1530	98.9	298	30	US-10-408-765A-1631	Sequence 1631, Ap
17	1530	98.9	298	32	US-09-389-987-1631	Sequence 1631, Ap
18	1530	98.9	298	32	US-09-412-418-1631	Sequence 1631, Ap
19	1530	98.9	320	22	US-09-760-469-1310	Sequence 1310, Ap
20	1530	98.9	320	28	US-10-216-583-1310	Sequence 1310, Ap
21	1454	94.0	298	1	PCT-US01-15416-32	Sequence 32, Appl
22	1454	94.0	298	15	US-09-185-904A-33	Sequence 33, Appl
23	1454	94.0	298	17	US-09-393-441-33	Sequence 33, Appl
24	1454	94.0	298	18	US-09-488-725A-2786	Sequence 2786, Ap
25	1454	94.0	298	19	US-09-569-327-6	Sequence 6, Appl
26	1454	94.0	298	21	US-09-709-785-49	Sequence 49, Appl
27	1454	94.0	298	23	US-09-809-889-33	Sequence 33, Appl
28	1454	94.0	298	23	US-09-809-889-33	Sequence 33, Appl
29	1454	94.0	298	23	US-09-810-644-33	Sequence 33, Appl
30	1454	94.0	298	23	US-09-811-094-33	Sequence 33, Appl
31	1454	94.0	298	23	US-09-811-132-33	Sequence 33, Appl
32	1454	94.0	298	28	US-10-258-898A-2786	Sequence 2786, Ap
33	1454	94.0	298	28	US-10-286-897-2786	Sequence 2786, Ap
34	1454	94.0	323	18	US-09-488-725A-6358	Sequence 6358, Ap
35	1454	94.0	323	28	US-10-258-898A-6358	Sequence 6358, Ap
36	1454	94.0	323	28	US-10-286-897-6358	Sequence 6358, Ap
37	1450	93.7	298	30	US-10-403-571-154	Sequence 154, App
38	1450	93.7	298	30	US-10-405-887-154	Sequence 154, App
39	1448	93.6	298	30	US-10-408-765A-2398	Sequence 2398, Ap
40	1448	93.6	298	32	US-09-389-987-2398	Sequence 2398, Ap
41	1448	93.6	298	32	US-09-412-418-2398	Sequence 2398, Ap
42	1417	91.6	325	1	PCT-US01-0631-45782	Sequence 45782, A
43	1413	91.3	298	30	US-10-408-765A-1680	Sequence 1680, Ap
44	1413	91.3	298	32	US-09-389-987-1680	Sequence 1680, Ap
45	1413	91.3	298	32	US-09-412-418-1680	Sequence 1680, Ap

#### ALIGNMENTS

RESULT 1  
PCT-US01-15416-32  
Sequence 32, Application PC/RUS0115416  
GENERAL INFORMATION:  
APPLICANT: Mitokor  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Cleverger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Willey, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
FILE REFERENCE: 660088.443PC  
CURRENT APPLICATION NUMBER: PCT/US01/15416  
CURRENT FILING DATE: 2001-05-11  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien

PCT-US01-15416-32

Query Match 100.0%; Score 1547; DB 1; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-159;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKQYGIIDCVR 60  
 DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKQYGIIDCVR 60  
 QY 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120  
 DB 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120  
 QY 121 GAAAGTSLCFYVPLDPARTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180  
 DB 121 GAAAGTSLCFYVPLDPARTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180  
 QY 181 VGGIITRAAYFGIYDTAKGMLPDKNTHIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240  
 DB 181 VGGIITRAAYFGIYDTAKGMLPDKNTHIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240  
 QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAMSNVLRGMGAFVLVYDEIKKTY 298  
 DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAMSNVLRGMGAFVLVYDEIKKTY 298

## RESULT 2

US-09-185-904A-32

Sequence 32, Application US/09185904A

GENERAL INFORMATION:  
 APPLICANT: Anderson, Christen M.  
 APPLICANT: Davis, Robert E.  
 APPLICANT: Clevenger, William  
 APPLICANT: Wiley, Sandra Eileen  
 APPLICANT: Miller, Scott W.  
 APPLICANT: Szabo, Tomas R.  
 APPLICANT: Ghosh, Soumitra S.  
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
 TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
 TITLE OF INVENTION: THEREFOR  
 FILE REFERENCE: 660088.420  
 CURRENT APPLICATION NUMBER: US/09/185,904A  
 CURRENT FILING DATE: 1998-11-03  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 32  
 LENGTH: 298  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-185-904A-32

Query Match 100.0%; Score 1547; DB 15; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-159;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKQYGIIDCVR 60  
 DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKQYGIIDCVR 60  
 QY 61 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120  
 DB 61 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120  
 QY 121 GAAAGTSLCFYVPLDPARTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180  
 DB 121 GAAAGTSLCFYVPLDPARTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180  
 QY 181 VGGIITRAAYFGIYDTAKGMLPDKNTHIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240  
 DB 181 VGGIITRAAYFGIYDTAKGMLPDKNTHIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240  
 QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAMSNVLRGMGAFVLVYDEIKKTY 298

DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAMSNVLRGMGAFVLVYDEIKKTY 298

## RESULT 3

US-09-393-441-32

Sequence 32, Application US/09393441  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, Christen M.  
 APPLICANT: Davis, Robert E.  
 APPLICANT: Clevenger, William  
 APPLICANT: Wiley, Sandra Eileen  
 APPLICANT: Miller, Scott W.  
 APPLICANT: Szabo, Tomas R.  
 APPLICANT: Ghosh, Soumitra S.  
 APPLICANT: Moos, Walter H.  
 APPLICANT: Pel, Yazheng  
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),  
 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 FILE REFERENCE: 660088.420C1  
 CURRENT APPLICATION NUMBER: US/09/393,441  
 CURRENT FILING DATE: 1999-09-08  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 32  
 LENGTH: 298  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-393-441-32

Query Match 100.0%; Score 1547; DB 17; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-159;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKQYGIIDCVR 60  
 DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKQYGIIDCVR 60  
 QY 61 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120  
 DB 61 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120  
 QY 121 GAAAGTSLCFYVPLDPARTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180  
 DB 121 GAAAGTSLCFYVPLDPARTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180  
 QY 181 VGGIITRAAYFGIYDTAKGMLPDKNTHIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240  
 DB 181 VGGIITRAAYFGIYDTAKGMLPDKNTHIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240  
 QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAMSNVLRGMGAFVLVYDEIKKTY 298  
 DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAMSNVLRGMGAFVLVYDEIKKTY 298

## RESULT 4

US-09-709-785-48

Sequence 48, Application US/09709785

GENERAL INFORMATION:  
 APPLICANT: Murphy, Anne N.  
 APPLICANT: Clevenger, William  
 APPLICANT: Wiley, Sandra Eileen  
 APPLICANT: Andreyev, Alexander Y.  
 APPLICANT: Frigeri, Luciano G.  
 APPLICANT: Velicelci, Gonul  
 APPLICANT: Davis, Robert E.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
 TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
 TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
 FILE REFERENCE: 660088.433C1  
 CURRENT APPLICATION NUMBER: US/09/709,785  
 CURRENT FILING DATE: 2002-09-16  
 NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 48  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-709-785-48

Query Match 100.0%; Score 1547; DB 21; Length 298;  
Best Local Similarity 100.0%; Pred. No. 2.9e-159;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAALSPADPLAGGVAALISKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVVR 60  
DB 1 MTDAALSPADPLAGGVAALISKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVVR 60  
QY 61 IPKQEVLSFWRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120  
DB 61 IPKQEVLSFWRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120  
QY 121 GAAGATSLCFYYPPLDFARTLADVKGAGAREBERGLDCLVKIYKSDGIGLYOGFNVS 180  
DB 121 GAAGATSLCFYYPPLDFARTLADVKGAGAREBERGLDCLVKIYKSDGIGLYOGFNVS 180  
QY 181 VGGIIRAAVFGIYDTAKGMLPDKNTHIVISWMIQVTAVALTSYFPDYRRRMM 240  
DB 181 VGGIIRAAVFGIYDTAKGMLPDKNTHIVISWMIQVTAVALTSYFPDYRRRMM 240  
QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGKAFPKGAMSVNLKMGCAFVLVYDEIKKYY 298  
DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGKAFPKGAMSVNLKMGCAFVLVYDEIKKYY 298

## RESULT 5

US-09-809-827-32  
Sequence 32, Application US/09809827  
GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pei, Yazhong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D6  
CURRENT APPLICATION NUMBER: US/09/809,827  
CURRENT FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-809-827-32

Query Match 100.0%; Score 1547; DB 23; Length 298;  
Best Local Similarity 100.0%; Pred. No. 2.9e-159;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAALSPADPLAGGVAALISKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVVR 60  
DB 1 MTDAALSPADPLAGGVAALISKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVVR 60  
QY 61 IPKQEVLSFWRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120  
DB 61 IPKQEVLSFWRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120  
QY 121 GAAGATSLCFYYPPLDFARTLADVKGAGAREBERGLDCLVKIYKSDGIGLYOGFNVS 180  
DB 121 GAAGATSLCFYYPPLDFARTLADVKGAGAREBERGLDCLVKIYKSDGIGLYOGFNVS 180

QY 161 VGGIIRAAVFGIYDTAKGMLPDKNTHIVISWMIQVTAVALTSYFPDYRRRMM 240  
DB 161 VGGIIRAAVFGIYDTAKGMLPDKNTHIVISWMIQVTAVALTSYFPDYRRRMM 240  
QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGKAFPKGAMSVNLKMGCAFVLVYDEIKKYY 298  
DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGKAFPKGAMSVNLKMGCAFVLVYDEIKKYY 298

## RESULT 6

US-09-809-889-32  
Sequence 32, Application US/09809889  
GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pei, Yazhong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D7  
CURRENT APPLICATION NUMBER: US/09/809,889  
CURRENT FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-809-889-32

Query Match 100.0%; Score 1547; DB 23; Length 298;  
Best Local Similarity 100.0%; Pred. No. 2.9e-159;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAALSPADPLAGGVAALISKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVVR 60  
DB 1 MTDAALSPADPLAGGVAALISKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVVR 60  
QY 61 IPKQEVLSFWRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120  
DB 61 IPKQEVLSFWRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120  
QY 121 GAAGATSLCFYYPPLDFARTLADVKGAGAREBERGLDCLVKIYKSDGIGLYOGFNVS 180  
DB 121 GAAGATSLCFYYPPLDFARTLADVKGAGAREBERGLDCLVKIYKSDGIGLYOGFNVS 180  
QY 181 VGGIIRAAVFGIYDTAKGMLPDKNTHIVISWMIQVTAVALTSYFPDYRRRMM 240  
DB 181 VGGIIRAAVFGIYDTAKGMLPDKNTHIVISWMIQVTAVALTSYFPDYRRRMM 240  
QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGKAFPKGAMSVNLKMGCAFVLVYDEIKKYY 298  
DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGKAFPKGAMSVNLKMGCAFVLVYDEIKKYY 298

## RESULT 7

US-09-810-644-32  
Sequence 32, Application US/09810644  
GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.

```

; APPLICANT: Pel, Yachong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32

```

```

Query Match      100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTDALSPAKDPLAGVAAAISKTAAPIERVYKLLQVQHASKQITADKQYGIIDCVVR 60
DB 1 MTDALSPAKDPLAGVAAAISKTAAPIERVYKLLQVQHASKQITADKQYGIIDCVVR 60
QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
DB 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPFATRLAADVGKAGAREFRGLDCLVKYKSGIGLVOGFNVS 180
DB 121 GAAGATSLCFYVPLDPFATRLAADVGKAGAREFRGLDCLVKYKSGIGLVOGFNVS 180
QY 181 VOGIIITYAAVFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSYPPDYVRRMM 240
DB 181 VOGIIITYAAVFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSYPPDYVRRMM 240
QY 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKGAAMSVLRMGGAFLVLYDEIKKYT 298
DB 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKGAAMSVLRMGGAFLVLYDEIKKYT 298

```

```

RESULT 8
US-09-811-094-32

```

```

; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleenger, William
; APPLICANT: Wile, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moes, Walter H.
; APPLICANT: Pel, Yachong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32

```

```

Query Match      100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTDALSPAKDPLAGVAAAISKTAAPIERVYKLLQVQHASKQITADKQYGIIDCVVR 60
DB 1 MTDALSPAKDPLAGVAAAISKTAAPIERVYKLLQVQHASKQITADKQYGIIDCVVR 60

```

```

QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
DB 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPFATRLAADVGKAGAREFRGLDCLVKYKSGIGLVOGFNVS 180
DB 121 GAAGATSLCFYVPLDPFATRLAADVGKAGAREFRGLDCLVKYKSGIGLVOGFNVS 180
QY 181 VOGIIITYAAVFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSYPPDYVRRMM 240
DB 181 VOGIIITYAAVFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSYPPDYVRRMM 240
QY 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKGAAMSVLRMGGAFLVLYDEIKKYT 298
DB 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKGAAMSVLRMGGAFLVLYDEIKKYT 298

```

```

RESULT 9
US-09-811-132-32

```

```

; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleenger, William
; APPLICANT: Wile, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moes, Walter H.
; APPLICANT: Pel, Yachong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D5
; CURRENT APPLICATION NUMBER: US/09/811,132
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-132-32

```

```

Query Match      100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTDALSPAKDPLAGVAAAISKTAAPIERVYKLLQVQHASKQITADKQYGIIDCVVR 60
DB 1 MTDALSPAKDPLAGVAAAISKTAAPIERVYKLLQVQHASKQITADKQYGIIDCVVR 60
QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
DB 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPFATRLAADVGKAGAREFRGLDCLVKYKSGIGLVOGFNVS 180
DB 121 GAAGATSLCFYVPLDPFATRLAADVGKAGAREFRGLDCLVKYKSGIGLVOGFNVS 180
QY 181 VOGIIITYAAVFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSYPPDYVRRMM 240
DB 181 VOGIIITYAAVFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSYPPDYVRRMM 240
QY 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKGAAMSVLRMGGAFLVLYDEIKKYT 298
DB 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKGAAMSVLRMGGAFLVLYDEIKKYT 298

```

```

RESULT 10
PCT-US02-01048-54
; Sequence 54, Application PC/TUS0201048
; GENERAL INFORMATION:
; APPLICANT: EXLIXIS, INC.

```

```

; TITLE OF INVENTION: Modulating Insulin Receptor Signaling
; FILE REFERENCE: EX02-001C-PC
; CURRENT APPLICATION NUMBER: PCT/US02/01048
; CURRENT FILING DATE: 2002-01-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-01048-54

Query Match          99.4% Score 1537; DB 1; Length 298;
Best Local Similarity 99.3% Pred. No. 3.5e-158;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAALISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
DB 1 MTDAAVSPAKDFLAGGVAALISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSAG 120
DB 61 IPKEQVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSAG 120
QY 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
DB 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
QY 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
DB 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
QY 181 VQGIITRYAAVFGIYDPAKGLPDPKNTHTIVISWMIQTVTAVALGLTSYPEDTVRRRMM 240
DB 181 VQGIITRYAAVFGIYDPAKGLPDPKNTHTIVISWMIQTVTAVALGLTSYPEDTVRRRMM 240
QY 241 QSGRKGIDIMYTGTLDCRKRLARDEGGAFFKGAMSNVLRMGAFVLVLYDEIKKYT 298
DB 241 QSGRKGIDIMYTGTLDCRKRLARDEGGAFFKGAMSNVLRMGAFVLVLYDEIKKYT 298

RESULT 11
US-09-569-327-5
; Sequence 5, Application US/09569327
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clewenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yezhong
; APPLICANT: Carroll, Amy K.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS
; TITLE OF INVENTION: AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.443
; CURRENT APPLICATION NUMBER: US/09/569.327
; CURRENT FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-569-327-5

Query Match          99.4% Score 1537; DB 19; Length 298;
Best Local Similarity 99.3% Pred. No. 3.5e-158;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAALISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
DB 1 MTDAAVSPAKDFLAGGVAALISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
```

```

QY 61 IPKEQVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSAG 120
DB 61 IPKEQVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSAG 120
QY 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
DB 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
QY 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
DB 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
QY 181 VQGIITRYAAVFGIYDPAKGLPDPKNTHTIVISWMIQTVTAVALGLTSYPEDTVRRRMM 240
DB 181 VQGIITRYAAVFGIYDPAKGLPDPKNTHTIVISWMIQTVTAVALGLTSYPEDTVRRRMM 240
QY 241 QSGRKGIDIMYTGTLDCRKRLARDEGGAFFKGAMSNVLRMGAFVLVLYDEIKKYT 298
DB 241 QSGRKGIDIMYTGTLDCRKRLARDEGGAFFKGAMSNVLRMGAFVLVLYDEIKKYT 298

RESULT 12
US-10-466-162-54
; Sequence 54, Application US/10466162
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling
; FILE REFERENCE: EX02-001C-PC
; CURRENT APPLICATION NUMBER: US/10/466,162
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 60/261,335
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,694
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,532
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,361
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,531
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,457
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,226
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,304
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,459
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,456
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-466-162-54

Query Match          99.4% Score 1537; DB 30; Length 298;
Best Local Similarity 99.3% Pred. No. 3.5e-158;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAALISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
DB 1 MTDAAVSPAKDFLAGGVAALISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
QY 61 IPKEQVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSAG 120
DB 61 IPKEQVLSFWRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSAG 120
QY 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
DB 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
QY 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
DB 121 GAAGATSLCFYYPPLDPARTRLAADVGKAGAREFRGIDCLVKIYKSDGIGLYOGFNV 180
QY 181 VQGIITRYAAVFGIYDPAKGLPDPKNTHTIVISWMIQTVTAVALGLTSYPEDTVRRRMM 240
```

Db 181 VGGIITRYAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGVTVAAGLTSYPTVRRMM 240  
 QY 241 QSGRKGTDIMYTGTLDCWKRKIARDGGAFFKGAWSNVLRGGAFLVLYDEIKKYT 298  
 Db 241 QSGRKGTDIMYTGTLDCWKRKIARDGGAFFKGAWSNVLRGGAFLVLYDEIKKYT 298

## RESULT 13

US-60-452-680-20286  
 ; Sequence 20286, Application US/60452680  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: GROPE, Andrew  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO01450  
 ; CURRENT APPLICATION NUMBER: US/60/452,680  
 ; CURRENT FILING DATE: 2003-03-07  
 ; NUMBER OF SEQ ID NOS: 116213  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 20286  
 ; LENGTH: 298  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-452-680-20286

Query Match 99.4%; Score 1537; DB 32; Length 298;  
 Best Local Similarity 99.3%; Pred. No. 3.5e-158;  
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQITADKQYGIIDCVR 60  
 Db 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQITADKQYGIIDCVR 60  
 QY 61 IPKQGVLSFMRGNLANVIRFPYQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120  
 Db 61 IPKQGVLSFMRGNLANVIRFPYQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120  
 QY 121 GAAGATSLCFYVPLDPARTRLAADVKGAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180  
 Db 121 GAAGATSLCFYVPLDPARTRLAADVKGAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180  
 QY 181 VGGIITRYAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGVTVAAGLTSYPTVRRMM 240  
 Db 181 VGGIITRYAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGVTVAAGLTSYPTVRRMM 240  
 QY 241 QSGRKGTDIMYTGTLDCWKRKIARDGGAFFKGAWSNVLRGGAFLVLYDEIKKYT 298  
 Db 241 QSGRKGTDIMYTGTLDCWKRKIARDGGAFFKGAWSNVLRGGAFLVLYDEIKKYT 298

## RESULT 14

US-09-760-469-1767  
 ; Sequence 1767, Application US/09760469  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROSEN et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PT254  
 ; CURRENT APPLICATION NUMBER: US/09/760,469  
 ; CURRENT FILING DATE: 2001-01-16  
 ; Prior Application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 1983  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1767  
 ; LENGTH: 332  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (8)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE

LOCATION: (11)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; US-09-760-469-1767

Query Match 99.4%; Score 1537; DB 22; Length 332;  
 Best Local Similarity 99.3%; Pred. No. 4.1e-158;  
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQITADKQYGIIDCVR 60  
 Db 35 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVHASKQITADKQYGIIDCVR 94  
 QY 61 IPKQGVLSFMRGNLANVIRFPYQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120  
 Db 95 IPKQGVLSFMRGNLANVIRFPYQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 154  
 QY 121 GAAGATSLCFYVPLDPARTRLAADVKGAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180  
 Db 155 GAAGATSLCFYVPLDPARTRLAADVKGAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 214  
 QY 181 VGGIITRYAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGVTVAAGLTSYPTVRRMM 240  
 Db 215 VGGIITRYAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGVTVAAGLTSYPTVRRMM 274  
 QY 241 QSGRKGTDIMYTGTLDCWKRKIARDGGAFFKGAWSNVLRGGAFLVLYDEIKKYT 298  
 Db 275 QSGRKGTDIMYTGTLDCWKRKIARDGGAFFKGAWSNVLRGGAFLVLYDEIKKYT 332

## RESULT 15

US-10-216-583-1767  
 ; Sequence 1767, Application US/10216583  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROSEN et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PT254C1N  
 ; CURRENT APPLICATION NUMBER: US/10/216,583  
 ; CURRENT FILING DATE: 2002-08-12  
 ; PRIOR APPLICATION NUMBER: 09/760,469  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: 60/179,065  
 ; PRIOR FILING DATE: 2000-01-31  
 ; PRIOR APPLICATION NUMBER: 60/180,628  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: 60/214,886  
 ; PRIOR FILING DATE: 2000-06-28  
 ; PRIOR APPLICATION NUMBER: 60/217,487  
 ; PRIOR FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: 60/225,758  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/220,963  
 ; PRIOR FILING DATE: 2000-07-26  
 ; PRIOR APPLICATION NUMBER: 60/217,496  
 ; PRIOR FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: 60/225,447  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/218,290  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 1983  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1767  
 ; LENGTH: 332  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (8)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (11)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids



US-10-216-583-1767

Query Match 99.4%; Score 1537; DB 28; Length 332;  
 Best Local Similarity 99.3%; Pred. No. 4.1e-158;  
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MTDAALSPAKDFLAGVAAAIKTAVAPIERVKLLLOVQHASKOITADKOYKGIIDCVVR	60
Db	35	MTDAALSPAKDFLAGVAAAIKTAVAPIERVKLLLOVQHASKOITADKOYKGIIDCVVR	94
Qy	61	IPKEQVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG	120
Db	95	IPKEQVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG	154
Qy	121	GAAGATSLCFVYPLDFAFRTLAADVGRGAERERFGLGDCLVKTKSDGIKGLYQGFNVS	180
Db	155	GAAGATSLCFVYPLDFAFRTLAADVGRGAERERFGLGDCLVKTKSDGIKGLYQGFNVS	214
Qy	181	VOGIIYRAAVFGIYDTAKGMLPDPKXTHIVISWMIAGTVAVAGLTSYPEDTVRRMM	240
Db	215	VOGIIYRAAVFGIYDTAKGMLPDPKXTHIVISWMIAGTVAVAGLTSYPEDTVRRMM	274
Qy	241	QSGRKGTDIMYTGTLDCWKRIARDEGGKAFPKGAMSNVLRMGGAFLVLYDEIKKYYT	298
Db	275	QSGRKGTDIMYTGTLDCWKRIARDEGGKAFPKGAMSNVLRMGGAFLVLYDEIKKYYT	332

Search completed: December 18, 2003, 12:53:25  
 Job time : 166.852 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:46 ; Search time 14.3494 Seconds  
(without alignments)  
1997.178 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547  
Sequence: 1 MTDALSPADFLAGVAA.....LRGKGAFVLVYDEIKYT 298

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1547	100.0	298	1 A29132	ADP,ATP carrier pr
2	1479	95.6	298	2 S31814	ADP,ATP carrier pr
3	1458	94.2	298	3 B43646	ADP,ATP carrier pr
4	1454	94.0	298	1 S03894	ADP,ATP carrier pr
5	1419	91.7	298	1 XMO	ADP,ATP carrier pr
6	1417	91.6	298	2 S37210	ADP,ATP carrier pr
7	1413	91.6	298	2 160173	adenine nucleotide
8	1413	91.3	298	1 A44778	ADP,ATP carrier pr
9	1170	75.6	301	1 S31935	ADP,ATP carrier pr
10	1032	66.7	300	2 T25371	hypothetical prote
11	1029	66.5	313	2 T23207	hypothetical prote
12	1029	66.5	313	2 T25850	hypothetical prote
13	986	63.7	300	2 T15206	ADP,ATP carrier pr
14	968	62.6	339	2 A41677	ADP,ATP carrier pr
15	938	60.6	301	2 S51132	ADP,ATP carrier pr
16	771	49.8	386	2 T09709	ADP,ATP carrier pr
17	770	49.8	386	2 T40526	ADP,ATP carrier pr
18	765	49.5	308	1 S30259	ADP,ATP carrier pr
19	761.5	49.1	307	2 A36582	ADP,ATP carrier pr
20	759	49.1	326	2 T25728	hypothetical prote
21	759	49.1	387	2 S14876	ADP,ATP carrier pr
22	757	48.9	313	1 XWNC	ADP,ATP carrier pr
23	754	48.7	386	2 S17917	ADP,ATP carrier pr
24	753	48.7	387	2 S15668	ADP,ATP carrier pr
25	752.5	48.6	318	1 A31978	ADP,ATP carrier pr
26	752	48.6	386	2 S21974	ADP,ATP carrier pr
27	749.5	48.4	305	2 S68154	ADP,ATP carrier pr
28	749.5	48.4	306	2 T20012	hypothetical prote
29	746	48.2	306	2 T42011	ADP,ATP carrier pr

30	746	48.2	379	2 T04608	ADP,ATP carrier pr
31	745.5	48.2	385	1 S29852	ADP,ATP carrier pr
32	745	48.2	382	2 S33630	ADP,ATP carrier pr
33	741.5	47.9	379	2 S21313	ADP,ATP carrier pr
34	741.5	47.9	386	2 S14874	ADP,ATP carrier pr
35	728	47.1	309	2 A24849	ADP,ATP carrier pr
36	665.5	43.0	298	2 T24029	hypothetical prote
37	521.5	33.7	327	2 T51577	ADP,ATP translocas
38	388	25.1	325	2 T04273	hypothetical prote
39	372	24.0	381	2 T51158	hypothetical prote
40	372	24.0	415	2 T48171	hypothetical prote
41	356	23.0	352	2 T01729	mitochondrial sol
42	350	22.6	475	2 T50686	peroxisomal Ca-dep
43	340	22.0	358	2 T45934	hypothetical prote
44	334	21.6	348	2 D84798	hypothetical prote
45	322.5	20.8	332	2 T47703	probable mitochon

## ALIGNMENTS

## RESULT 1

A29132  
ADP,ATP carrier protein T2 - human

N:Alternate names: mitochondrial ADP,ATP translocase 2

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000

C:Accession: A29132; C28116

R:Battini, R.; Ferrarini, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Basegga, R.

J. Biol. Chem. 262, 4355-4359, 1987

A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat

A:Reference number: A29132; MUID:87166056; PMID:3031073

A:Accession: A29132

A:Molecule type: mRNA

A:Residues: 1-298 <BAT>

A:Cross-references: GB:J02683; NID:G179246; PIDN:AAA35579.1; PID:G179247

R:Holdsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: C28116

A:Molecule type: mRNA

A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>

A:Cross-references: GB:J03551; NID:G339720; PIDN:AAA36749.1; PID:G339721

A:Experimental source: Clone pBAT3

C:Genetics:

A:Gene: GDB:ANT2; T3; 2F1

A:Cross-references: GDB:125190; OMIM:300150

A:Map position: Xq13-Xq26

A>Note: There may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrial; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <AC2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <AC3>

Query Match 100.0%; Score 1547; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 4e-130;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTDALSPADFLAGVAAAIKSTNAVPIREVKLLIQVHASKQITADKQYKGIIDCVNR	60
DB	1	MTDALSPADFLAGVAAAIKSTNAVPIREVKLLIQVHASKQITADKQYKGIIDCVNR	60
QY	61	IPKQEVLSFPRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFMFVFAGNLASG	120
DB	61	IPKQEVLSFPRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFMFVFAGNLASG	120
QY	121	GAAGATSLCFYVPIIDFATRIADVGKAGAEERFGAGDCIVKIKSDGIGKLYQGFNVS	180
DB	121	GAAGATSLCFYVPIIDFATRIADVGKAGAEERFGAGDCIVKIKSDGIGKLYQGFNVS	180
QY	181	VOGIIITPAALFGLYDRAKGLPDPKXTHIVISMIMIAQTVAVAGLTSYPPDYTRRRMM	240
DB	181	VOGIIITPAALFGLYDRAKGLPDPKXTHIVISMIMIAQTVAVAGLTSYPPDYTRRRMM	240

Db 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSPEDTVARRMM 240

Qy 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKKYT 298

Db 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKKYT 298

## RESULT 2

ADP, ATP carrier protein T2 - mouse  
 N:Alternate names: adenine nucleotide translocase  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Apr-1998  
 C:Accession: S31814  
 R:Coates, P.; Laplace, C.  
 Submitted to the EMBL Data Library, January 1993  
 A:Reference number: S31814  
 A:Accession: S31814  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-298 <COS>  
 A:Cross-references: EMBL:X70847  
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C:Keywords: duplication; transmembrane protein  
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>  
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 95.6%; Score 1479; DB 2; Length 298;  
 Best Local Similarity 95.6%; Pred. No. 4, 5e-124;  
 Matches 285; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIKTAIVAPIERVKLLIQVQASKOITADKQYKGIIDCYVR 60

Db 1 MTDAAISPAKDFLAGVAAAIKTAIVAPIERVKLLIQVQASKOITADKQYKGIIDCYVR 60

Qy 61 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120

Db 61 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120

Qy 121 GAAGATSLCFVYPLDPAFTRILADVGKAGREBFGDGLCVTKYKSGIKGLYGGFNVS 180

Db 121 GAAGATSLCFVYPLDPAFTRILADVGKAGREBFGDGLCVTKYKSGIKGLYGGFNVS 180

Qy 121 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSPEDTVARRMM 240

Db 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSPEDTVARRMM 240

Qy 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKKYT 298

Db 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKKYT 298

## RESULT 3

ADP, ATP carrier protein T2 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 20-Aug-1999  
 C:Accession: B43646  
 R:Powell, S.J.; Wedd, S.M.; Runswick, M.J.; Walker, J.E.  
 Biochemistry 28, 866-873, 1989  
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
 A:Reference number: B43646; MUID:89229093; PMID:2540808  
 A:Accession: B43646  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-298 <POM>  
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417  
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C:Keywords: duplication; homodimer; mitochondrial; transmembrane protein  
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1458; DB 2; Length 298;  
 Best Local Similarity 92.9%; Pred. No. 3, 4e-122;  
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIKTAIVAPIERVKLLIQVQASKOITADKQYKGIIDCYVR 60

Db 1 MTDAAISPAKDFLAGVAAAIKTAIVAPIERVKLLIQVQASKOITADKQYKGIIDCYVR 60

Qy 61 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120

Db 61 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120

Qy 121 GAAGATSLCFVYPLDPAFTRILADVGKAGREBFGDGLCVTKYKSGIKGLYGGFNVS 180

Db 121 GAAGATSLCFVYPLDPAFTRILADVGKAGREBFGDGLCVTKYKSGIKGLYGGFNVS 180

Qy 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSPEDTVARRMM 240

Db 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAVAGLTSPEDTVARRMM 240

Qy 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKKYT 296

Db 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKKYT 296

## RESULT 4

ADP, ATP carrier protein T3 - human  
 N:Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP, ATP  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C:Accession: S03894; B28116  
 R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.  
 J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr  
 A:Reference number: S03893; MUID:8923696; PMID:2541251  
 A:Accession: S03894

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <COS>

R:Holdsworth, J.; Attardi, G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: B28116

A:Molecule type: mRNA

A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>

A:Cross-references: GB:J03592; NID:9339722; PIDN:AAA36750.1; PID:9339723

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT3; ANT3X

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3

A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrial; transmembrane protein

F:2-398/Product: ADP, ATP carrier protein #status predicted <MNT>

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.0%; Score 1454; DB 1; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 7, 6e-122;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIKTAIVAPIERVKLLIQVQASKOITADKQYKGIIDCYVR 60

Db 1 MTDAAISPAKDFLAGVAAAIKTAIVAPIERVKLLIQVQASKOITADKQYKGIIDCYVR 60

Qy 61 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120

Db 61 IPKEQVLSFWRGMLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
Qy 121 GAAGATSLCFVYPLDPFARTLADVGKAGBERBGLGDCIVKTKYSGIGLYQGFNV 180  
Db 121 GAAGATSLCFVYPLDPFARTLADVGKAGBERBGLGDCIVKTKYSGIGLYQGFNV 180  
Qy 181 VGGIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPTDVRBRMM 240  
Db 181 VGGIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPTDVRBRMM 240  
Qy 241 QSGRKGTDIMYTGTLDCWRKIADDEGKAFPKGAMSVNLKMGGAFLVLYDEIKK 296  
Db 241 QSGRKGADIMYTGTLDCWRKIADDEGKAFPKGAMSVNLKMGGAFLVLYDEIKK 296

RESULT 5

WBO  
ADP, ATP carrier protein T1 - bovine  
N/Alternate names: ADP/ATP translocase T1  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 14-Nov-1993 #sequence\_revision 22-Jul-1994 #text\_change 22-Jun-1999  
A/Accession: A43646; A24822; A03181; A61343; S63369  
R/Powell, S.J.; Medd, S.M.; Rumsack, M.J.; Walker, J.R.  
Biochemistry 28, 866-873, 1989  
A/Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
A/Reference number: A43646; MUID:89229093; PMID:2540808  
A/Accession: A43646  
A/Molecule type: mRNA  
A/Residues: 1-298 <POM>  
A/Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415  
R/Rasmussen, U.B.; Mohlirab, H.  
Biochem. Biophys. Res. Commun. 138, 850-857, 1986  
A/Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual  
A/Reference number: A24822; MUID:86295775; PMID:3017341  
A/Accession: A24822  
A/Molecule type: mRNA  
A/Residues: 208-298 <RAS>  
A/Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631  
R/Aquila, H.; Mista, D.; Bullitz, M.; Klingenberg, M.  
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982  
A/Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria  
A/Reference number: A03181; MUID:82188267; PMID:7076130  
A/Accession: A03181  
A/Molecule type: protein  
A/Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AGU>  
A/Note: residue 52 may be methyllysine  
R/Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.  
Biochim. Biophys. Acta 670, 176-180, 1981  
A/Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitoch  
A/Reference number: A61343; MUID:82046808; PMID:6271240  
A/Accession: A61343  
A/Molecule type: protein  
A/Residues: 205-298 <BAB>  
R/Oetmeier, W.; Masson, K.; Kalina, S.  
Eur. J. Biochem. 227, 730-733, 1995  
A/Title: [(3)H]-azido-4-isopropylazidione labels Cys159 of the bovine mitochondrial ADP  
A/Reference number: S69369; MUID:95172058; PMID:7867632  
A/Accession: S69369  
A/Molecule type: protein  
A/Residues: 49-63, 154-168 <OET>  
A/Comment: This protein is synthesized in the cytosol and transported into the mitochondr  
C/Complex: homodimer  
C/Function:  
A/Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera  
A/Note: located in the inner mitochondrial membrane  
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
C/Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch  
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>  
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental  
F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 91.7%; Score 1419; DB 1; Length 298;  
Best Local Similarity 89.9%; Pred. No. 1e-118;  
Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MTDALSPADFLAGVAAAIKTAIVAPIRVKLLQVHASKQITADKQYKGIIDCV 60  
Db 1 MSDQALSFLLDFLAGVAAAIKTAIVAPIRVKLLQVHASKQISAEKQYKGIIDCV 60  
Qy 61 IPKEQVLSFWRGMLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
Db 61 IPKEQVLSFWRGMLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
Qy 121 GAAGATSLCFVYPLDPFARTLADVGKAGBERBGLGDCIVKTKYSGIGLYQGFNV 180  
Db 121 GAAGATSLCFVYPLDPFARTLADVGKAGBERBGLGDCIVKTKYSGIGLYQGFNV 180  
Qy 181 VGGIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPTDVRBRMM 240  
Db 181 VGGIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPTDVRBRMM 240  
Qy 241 QSGRKGTDIMYTGTLDCWRKIADDEGKAFPKGAMSVNLKMGGAFLVLYDEIKK 297  
Db 241 QSGRKGADIMYTGTLDCWRKIADDEGKAFPKGAMSVNLKMGGAFLVLYDEIKK 297

RESULT 6

S37210  
ADP, ATP carrier protein T1 - mouse  
N/Alternate names: adenine nucleotide carrier  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999  
A/Accession: S37210  
R/Laplace, C.; Costet, P.  
submitted to the EMBL Data Library, September 1993  
A/Reference number: S37210  
A/Accession: S37210  
A/Molecule type: preliminary  
A/Status: preliminary  
A/Residues: 1-298 <LAP>  
A/Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628  
C/Genetics:  
A/Gene: ANCL  
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
C/Keywords: duplication; transmembrane protein  
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.6%; Score 1417; DB 2; Length 298;  
Best Local Similarity 89.6%; Pred. No. 1.5e-118;  
Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTDALSPADFLAGVAAAIKTAIVAPIRVKLLQVHASKQITADKQYKGIIDCV 60  
Db 1 MGDQALSFLLDFLAGVAAAIKTAIVAPIRVKLLQVHASKQISAEKQYKGIIDCV 60  
Qy 61 IPKEQVLSFWRGMLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
Db 61 IPKEQVLSFWRGMLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
Qy 121 GAAGATSLCFVYPLDPFARTLADVGKAGBERBGLGDCIVKTKYSGIGLYQGFNV 180  
Db 121 GAAGATSLCFVYPLDPFARTLADVGKAGBERBGLGDCIVKTKYSGIGLYQGFNV 180  
Qy 181 VGGIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPTDVRBRMM 240  
Db 181 VGGIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPTDVRBRMM 240  
Qy 241 QSGRKGTDIMYTGTLDCWRKIADDEGKAFPKGAMSVNLKMGGAFLVLYDEIKK 297  
Db 241 QSGRKGADIMYTGTLDCWRKIADDEGKAFPKGAMSVNLKMGGAFLVLYDEIKK 297

## RESULT 7

160173

adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999

C:Accession: 160173

R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A:Reference number: 160173; MUID:94002161; PMID:8399300

A:Accession: 160173

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 &lt;RES&gt;

A:Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA43842.1; PID:9400427

C:Genetics:

A:Gene: anti

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:110-202/Domain: ADP/ATP carrier protein repeat homology &lt;ACP2&gt;

F:207-298/Domain: ADP/ATP carrier protein repeat homology &lt;ACP3&gt;

Query Match 91.6%; Score 1417; DB 2; Length 298;

Best Local Similarity 89.6%; Pred. No. 1.5e-118;

Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAATSKTAVAPERVKLLQVQHSKQITADKQYKGIIDCVRR 60

DB 1 MGDHALSPKDFLAGVAAATSKTAVAPERVKLLQVQHSKQISAEKQYKGIIDCVRR 60

QY 61 IPKEQEVLSFMRGNLANIYRFPQTALNFAFDKTKQKIFLGVDKRTQFMRYPAGNLASG 120

DB 61 IPKEGGLSFMRGNLANIYRFPQTALNFAFDKTKQKIFLGVDKHKQFMRYPAGNLASG 120

QY 121 GAAGATSTCFYPPDPAFTRIALADYKGAERFEGDGLVTKYKSDIGLQYGFNVN 180

DB 121 GAAGATSTCFYPPDPAFTRIALADYKGAERFEGDGLVTKYKSDIGLQYGFNVN 180

QY 181 VGGIIITPAAYFGYIDTKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDVARRRMM 240

DB 181 VGGIIITPAAYFGYIDTKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDVARRRMM 240

QY 241 QSGRGKTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVLYDEIKKY 297

DB 241 QSGRGKADIMYTGTVDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVLYDEIKKY 297

## RESULT 8

A44778

ADP/ATP carrier protein T1 - human

N:Alternate names: mitochondrial ADP/ATP translocase 1

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000

C:Accession: A44778; S03893; A39891; A28116

R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.

J. Biol. Chem. 264, 13998-14004, 1999

A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located

A:Reference number: A44778; MUID:89340499; PMID:2547778

A:Accession: A44778

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 &lt;LIA&gt;

A:Cross-references: GB:J04982; NID:9178658; PIDN:AAA51736.1; PID:9178659

R:Cozens, A.L.; Kuniswick, M.O.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr

A:Reference number: S03893; MUID:89236396; PMID:2541251

A:Accession: S03893

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 &lt;COZ&gt;

R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.

Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987

A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader

A:Reference number: A39891; MUID:88041149; PMID:2823266

A:Accession: A39891

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 &lt;NEC&gt;

A:Cross-references: GB:J02966; NID:9339919; PIDN:AAA61233.1; PID:9339920

A:Experimental source: clone pHMAN7

R:Houldsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: A28116

A:Molecule type: mRNA

A:Residues: 1-37 &lt;HOV&gt;

A:Cross-references: GB:J03593; NID:9339724; PIDN:AAA6751.1; PID:9339725

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT1; T1

A:Cross-references: GDB:119680; OMIM:103220

A:Map position: 4q35-4q35

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:2-298/Product: ADP/ATP carrier protein #status predicted &lt;MNT&gt;

F:5-99/Domain: ADP/ATP carrier protein repeat homology &lt;ACP1&gt;

F:110-202/Domain: ADP/ATP carrier protein repeat homology &lt;ACP2&gt;

F:207-298/Domain: ADP/ATP carrier protein repeat homology &lt;ACP3&gt;

Query Match 91.3%; Score 1413; DB 1; Length 298;

Best Local Similarity 89.2%; Pred. No. 3.4e-118;

Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAATSKTAVAPERVKLLQVQHSKQITADKQYKGIIDCVRR 60

DB 1 MGDHALSPKDFLAGVAAATSKTAVAPERVKLLQVQHSKQISAEKQYKGIIDCVRR 60

QY 61 IPKEQEVLSFMRGNLANIYRFPQTALNFAFDKTKQKIFLGVDKRTQFMRYPAGNLASG 120

DB 61 IPKEGGLSFMRGNLANIYRFPQTALNFAFDKTKQKIFLGVDKHKQFMRYPAGNLASG 120

QY 121 GAAGATSTCFYPPDPAFTRIALADYKGAERFEGDGLVTKYKSDIGLQYGFNVN 180

DB 121 GAAGATSTCFYPPDPAFTRIALADYKGAERFEGDGLVTKYKSDIGLQYGFNVN 180

QY 181 VGGIIITPAAYFGYIDTKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDVARRRMM 240

DB 181 VGGIIITPAAYFGYIDTKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDVARRRMM 240

QY 241 QSGRGKTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVLYDEIKKY 297

DB 241 QSGRGKADIMYTGTVDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVLYDEIKKY 297

## RESULT 9

S31935

ADP/ATP carrier protein - African malaria mosquito

C:Species: Anopheles gambiae (African malaria mosquito)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S31935; S31936

R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.

submitted to the EMBL Data Library, February 1993

A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.

A:Reference number: S31935

A:Accession: S31935

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-301 &lt;BEA&gt;

A:Cross-references: EMBL:Z21814; EMBL:Z21815

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:7-101/Domain: ADP/ATP carrier protein repeat homology &lt;ACP1&gt;

F;112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F;209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match	75.6%;	Score 1170;	DB 1;	Length 301;
Best Local Similarity	78.1%;	Pred. No. 1.5e-96;		
Matches 225; Conservative	18;	Mismatches 45;	Indels 0;	Gaps 0

Qy 8 FADDFLAGGAAAIKSTAAVAFIERVELLQVQHAQKQITLADKQYGGIIDDVLRPEKEQEV 67

Db 10 FADDFLAGGISAASVSTAFAVAFIERVELLQVQAAKQIANDKQYGIYDCCVLRPEKQGI 69

Qy 68 LSTRRGKLANVIRYPTQALNFAFKDKYKQITLGGVDKTRQPMRYFAGNTLASGGAAGATS 127

Db 70 GAFQGGNLANVIRYPTQALNFAFKDKYVQVLELGGVDKTRQPMRYFLNLTGSGGAAGATS 129

Qy 128 LCFEYVPLDFAFRTLADVCGKAGAREFRGJGCLVKIKYKDOIKQLYQGFNVSVQGIITV 187

Db 130 LCFYVPLDFAFRTLADVCGKAGERRFRNGJLCLKTKYKSDBIIGLTRGFNVSVQGIITV 189

Qy 188 RAAVFGIYDTAKGMLDPPKNTHTIVISWMLAQTVTAVAGLTSYPPDVTARRMMQSGRGKT 247

Db 190 RAAVFGCFDTAKGMLDPPKNTSIFPVSWMLAQVVTVAAGTISPEFDTVRRMMQSNPKCS 249

Qy 248 DIATYGLDQWRKIALDEBGGKAFPGKAMSNVLRMGKGFATVLDVDEK 295

Db 250 EIVTKNTLDCSWVILGQKQBSGAEPKAFNSNVLRGGQALVLFVDVDEK 297

RESULT 10  
T25371

hypothetical protein T27E9.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C:Accession: T25371

Query Match	Score	DB 2	Length	300
66.7%	1032			

Rebet Local Similarity 69.8%; Pred. No. 2.9e-84; Matches 203; Conservative 34; Mismatched - 50; Indels 4; Gaps 3

	Qy	Db	Qy	Db	Qy	Db	Qy	Db
8	FADPFLAGVAAASKTAVAPERVKLLQVOHASKOITADQYKGIIDCVIRIPKEOV	67	68	LSPFRGNLANVI RYPTQALNFAFYDOKYKOIFLGSVDKRTOFWRFAGNLASGGAAGATS	127	72	AALMRGNLANVI RYPTQAMNFAPDYTKAITLBEGDDKKDPWKFPAAGNLASGGAAGATS	131
12	FLIDLASGRTAAASKIIVAPIERVKLLQVOODASKALAVDRKYGVINDVLIRVPEQGV	71	128	LCFVYPPLDFEARTRLAADVGAKAEREFRGLGDCLVIKYKSDIKGLYOGFNVSYOGII IY	187	132	LCFVYPPLDFEARTRLAADIGKAN-DREPKGLADCLIKIYKSDGPILGYGFVYSOGII IY	190
188	RAAFRGITDKAGML-PDPKNTHIYISMWIACTVTVAAGLSYFPDYTVRRMMOSGRKG	246	191	RAAFYGMEDTIKMVFASDGOKIINFPAANGIAQVVTVSGSIIISTYPMDTVRRRMMOSGRK-	249	247	TDIMWTGLDCMKRIARDEGGKAFFPKGMSNYLRBGWGAFVYLVLDELRIKKY	297
250	-DLFKNTLTDCARKKITIQNEGMSAMFRGALSINFRGTGVALTAIYADELSIQKF	299						

## RESULT 11

hypothetical protein K01H12.2 - *Caenorhabditis elegans*

C:\Species: Caenorhabditis elegans  
C:\Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C:\Accession: T23207  
R:\McMurray, A.

Query Match	66.5%	Score 1029;	DB 2;	length 313;
Best Local Similarity	70.8%;	Pred. No. 5.6e-84;		
Matches 206;	Conservative 28;	Mismatches 53;	Indels 4;	Gaps 3;

QY 8 FADDFLAGVAAAIKSTAAPIERKYLLOVQVHASKOLTADKOYKGIIDCVLRPEQEV 67

QY 25 FLIDLASGGTAANAVENTAPIERKYLLOVQVDSLTITADKRRKGIIDVULVVRPEQGY 84

QY 68 LSFWRGNLANVIRYPTQALNFAFDKYKQIPLGQVDRKTFQWRYFAGNLASGGAGATS 127

Db 85 AALMRGNLANVIRYPTQALNFAFDKYKNIPOKGLDKKQFMKRFAGNLASGGAGATS 144

QY 128 LCFVYPLDPAFTRTLADYQKAGABEPRGLDQC.VKLYKSDGIGLQGFNVSVQGIITV 187

Db 145 LCFVYPLDPAFTRTLADYQKAN-EREFGLDCLVKYLAKSDGIPGLRGPVSVQGIITV 203

QY 188 RAAVFGIYDTAKGM-PPDKNTHIVISWIAQVTAAGLTSYDPTVRRRMQSGRG 246

Db 204 RAAVFGMPTALNVFLADCKLNFPAALAIQVTVVSGIISTYPMPTVRRRMQSGRK- 262

QY 247 TDIMTYGLTDCWRKTLARQGGKAPFKGMSVULVGMGAPVULVYDSDIKXX 297

Db 263 -DVLVKNYLTDCAVKTIKNBGSANMKGLSVNFGTGGALVLAIYDSDIQRF 312

RESULT 12  
T25850

hypothetical protein T01B1.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C:Accession: T25850

Query Match	66.5%	Score 1029;	DB 2;	length 313;
Best Local Similarity	70.8%	Pred. No. 5.6e-84;		
Matches 206;	Conservative 28;	Mismatches 53;	Indels 4;	Gaps 3;



QY 8 FAKDPLAGVAAAIKSTAVAPIERVKLLIQVHASKQITADKQYKGIIDCVIRIPKEDEV 67  
 DB 25 FLIDLASGGTAASVSTAVAPIERVKLLIQVHASKQITADKQYKGIIDCVIRIPKEDEV 84  
 QY 68 LSPFMGNLANVIRYPTQALNFAFDKQYKQIFLGVDKRTQFWRFPAGNLASGGAAGTSS 127  
 DB 85 AALMNGNLANVIRYPTQALNFAFDKQYKQIFLGVDKRTQFWRFPAGNLASGGAAGTSS 144  
 QY 128 LCFVVPPLDPARTRLADVKGAEERFGLDCLVYKSDGIKGLYOGFNVSVGGIIT 187  
 DB 145 LCFVVPPLDPARTRLADVKGAEERFGLDCLVYKSDGIGLYRGGFVSVGGIIT 203  
 QY 188 RAAVYGIYDTAKGML-PDPKNTHTVISMIAQTVTAAGLTSYPTDTRRRMMQSGRKG 246  
 DB 204 RAAVYGMEDTAKVFTADGKINFPAAVIAQVTVVSGGISLSPYDTRRRMMQSGRKG- 262  
 QY 247 TDIMVTGTLDCWRKIARDEGKAFPKGAMSNVLRGAGAFVVLVDEIKCY 297  
 DB 263 -DVLKNTLDCVAKIKKGGMSMKGALSNVPRGTGALVLAIDELQKF 312

## RESULT 13

T15206

hypotheetical protein W02D3.6 - Caenorhabditis elegans

CSpecies: Caenorhabditis elegans

CDate: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jan-2000

CAccession: T15206

Riley, T.; Weinstein, L.; Rifkin, L.

submitted to the EMBL Data Library, May 1997

A.Description: The sequence of C. elegans cosmid W02D3.

A.Reference number: Z18308

A.Accession: T15206

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-300 &lt;LEP&gt;

A.Cross-references: EMBL:AF003141; NID:G2088732; PID:G2088738; PIDN:AA854179.1; GSPDB:GN

A.Experimental source: strain Bristol NZ; clone W02D3

C.Genetic: 1

A.Gene: CESP:W02D3.6

A.Map position: 1

C.Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

F:9-103/Domain: ADP, ATP carrier protein repeat homology &lt;ACR&gt;

Query Match 63.7%; Score 986; DB 2; Length 300;

Best Local Similarity 67.5%; Pred. No. 3.6e-80;

Matches 195; Conservative 32; Mismatches 58; Indels 4; Gaps 3;

QY 8 FAKDPLAGVAAAIKSTAVAPIERVKLLIQVHASKQITADKQYKGIIDCVIRIPKEDEV 67  
 DB 12 FLVDLASGGTAASVSTAVAPIERVKLLIQVSDVSEVTYADKKYKIMDLARVPEQCY 71  
 QY 68 LSPFMGNLANVIRYPTQALNFAFDKQYKQIFLGVDKRTQFWRFPAGNLASGGAAGTSS 127  
 DB 72 AAFMGNLANVIRYPTQALNFAFDKQYKQIFLGVDKRTQFWRFPAGNLASGGAAGTSS 131  
 QY 128 LCFVVPPLDPARTRLADVKGAEERFGLDCLVYKSDGIKGLYOGFNVSVGGIIT 187  
 DB 132 LCFVVPPLDPARTRLADVKGAEERFGLDCLVYKSDGIKGLYOGFNVSVGGIIT 190  
 QY 188 RAAVYGIYDTAKGML-PDPKNTHTVISMIAQTVTAAGLTSYPTDTRRRMMQSGRKG 246  
 DB 191 RAAVYGMEDTAKVFTADGKINFPAAVIAQVTVVSGGISLSPYDTRRRMMQSGRKG- 249  
 QY 247 TDIMVTGTLDCWRKIARDEGKAFPKGAMSNVLRGAGAFVVLVDEIKCY 295  
 DB 250 -DVLKNTLDCVAKIKKGGMSMKGALSNVPRGTGALVLAIDELQ 297

## RESULT 14

A41677

ADP, ATP carrier protein - Chlorella keesleri

CSpecies: Chlorella keesleri

CDate: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999

C.Accession: A41677  
 R.Hilgath, C./ Sauer, N.; Tanner, W.  
 J. Biol. Chem. 266, 24044-24047, 1991  
 A.Title: Glucose increases the expression of the ATP/ADP translocator and the glyceralde  
 A.Reference number: A41677; MUID:92084708; PMID:1748677  
 A.Accession: A41677  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-339 <HIL>  
 A.Cross-references: GB:M76669; NID:9516596; PIDN:AAA31027.1; PID:9516597  
 C.Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C.Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F:144-235/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
 F:241-329/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 62.6%; Score 988; DB 2; Length 339;

Best Local Similarity 65.8%; Pred. No. 1.7e-78;

Matches 194; Conservative 29; Mismatches 64; Indels 8; Gaps 5;

QY 6 LSPAFDLAGVAAAIKSTAVAPIERVKLLIQVHASKQITADK-QYKGIIDCVIRIPK 63  
 DB 39 MAFVYDLAGGTAGAIKSTAVAPIERVKLLIQVDSNPMKSGQVPRYTGIVNCFVRSS 98  
 QY 64 EOBVLSPFRGNLANVIRYPTQALNFAFDKQYKQIFLGVDKRTQFWRFPAGNLASGGA 123  
 DB 99 EOGVASFWRGNLANVIRYPTQALNFAFDKQYKQIFLGVDKRTQFWRFPAGNLASGGA 157  
 QY 124 GATSLCFYPLDPARTRLADVKGAEERFGLDCLVYKSDGIKGLYOGFNVSVGG 183  
 DB 158 GAGSLIYVPLDPARTRLADVKGAEERFGLDCLVYKSDGIKGLYOGFNVSVGG 216  
 QY 184 IIRYAAVYGIYDTAKGML-PDPKNTHTVISMIAQTVTAAGLTSYPTDTRRRMMQSG 242  
 DB 217 IIRYAAVYGIYDTAKGML-PDPKNTHTVISMIAQTVTAAGLTSYPTDTRRRMMQSG 276  
 QY 243 GRKGTIDMTGTLDCWRKIARDEGKAFPKGAMSNVLRGAGAFVVLVDEIKCY 297  
 DB 277 --GGRQYNGTIDCWRKIARDEGKAFPKGAMSNVLRGAGAFVVLVDEIKCY 328

## RESULT 15

S51132

ADP, ATP carrier protein - malaria parasite (Plasmodium falciparum)

N/Alternate names: ADP/ATP transporter

CSpecies: Plasmodium falciparum

CDate: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jun-2000

C.Accession: S58993; S51132

R.Hacin, I.; Dureguberry, G.

Eur. J. Biochem. 228, 86-91, 1995

A.Title: Molecular characterization of the ADP/ATP transporter cDNA from the human malar

A.Reference number: S58993; MUID:95186918; PMID:7883016

A.Accession: S58993

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-501 &lt;HAT&gt;

A.Cross-references: EMBL:X83551; NID:9623334; PIDN:CA58541.1; PID:9623335

C.Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C.Keywords: duplication; transmembrane protein

F:6-102/Domain: ADP, ATP carrier protein repeat homology &lt;ACPI&gt;

F:112-203/Domain: ADP, ATP carrier protein repeat homology &lt;ACP2&gt;

F:209-301/Domain: ADP, ATP carrier protein repeat homology &lt;ACP3&gt;

Query Match 60.6%; Score 938; DB 2; Length 301;

Best Local Similarity 61.2%; Pred. No. 6.8e-76;

Matches 183; Conservative 43; Mismatches 67; Indels 6; Gaps 5;

QY 2 TDAALSPAKDPLAGVAAAIKSTAVAPIERVKLLIQVHASKQITAD-KQYKGIIDCV 59  
 DB 3 SDIKTNPAADFLMGIASIKSTVPTIERVKMLIQVDSNPMKSGQVPRYTGIVNCFVRSS 62  
 QY 60 RIRKQGVLSFWRGNLANVIRYPTQALNFAFDKQYKQIFLGVDKRTQFWRFPAGNLAS 119

```

Db      63 RVSKEQVLSLRGNVANVIRYFPTQAFNFAKDYFNIF-PRYDQNTDFSKFCVNILS 121
QY      120 GGAAGATSLCFYYPIDFPAETRIAADVKGAGAEERERGLDCLVKYKSDGIKGLYQGFNV 179
Db      122 GATGAGATSLILVYPIDFPAETRIASDYGK-GKDRQFTGLPDCIAKLYKQIGLSLISGFGV 180
QY      180 SVQGIITIRAAVFGIYDTAKGML-PDPKNTNIVISMTIAQVTAVAGLTSYFPDTRRRM 238
Db      181 SVTGIIVRGSYFGIYDSKALLFTNDKNTNIVLKNVAVASVTIAGLISYFPDTRRRM 240
QY      239 MMQGRKG-TDIMYTGTLDCWRKLIARDEGKAFPGANSNVLKMGGAFLVLVYDEIKK 296
Db      241 MMMSGRKGEKBIQYKNTIDCWIKILRNBSGFKGFPKGAMNANVIRGAGALVLVYDELOK 299

```

Search completed: December 18, 2003, 12:44:04  
 Job time : 14.3494 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:36:16 ; Search time 8.34267 Seconds  
(without alignments)  
1679.794 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547

Sequence: 1 MTDALSPAKPLAGVAA.....LRNGGAFVLYVDEIKKYT 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	99.4	298	1	ADT2_HUMAN
2	1525	98.6	298	1	ADT2_RAT
3	1519	98.2	298	1	ADT2_MOUSE
4	1458	94.2	298	1	ADT3_BOVIN
5	1454	94.0	298	1	ADT3_HUMAN
6	1417	91.6	298	1	ADT1_MOUSE
7	1417	91.6	298	1	ADT1_RAT
8	1414	91.4	297	1	ADT1_BOVIN
9	1413	91.3	298	1	ADT1_HUMAN
10	1253.5	81.0	299	1	ADT_DROME
11	1190	76.9	301	1	ADT_ANOGA
12	968	62.6	339	1	ADT_CHLKE
13	771	49.8	386	1	ADT1_GOSHI
14	770	49.8	322	1	ADT_SCHPO
15	765	49.5	308	1	ADT_CHLRE
16	761.5	49.2	307	1	ADT3_YEAST
17	759	49.1	387	1	ADT1_MAIZE
18	757	48.9	313	1	ADT_NEUCR
19	753.5	48.7	385	1	ADT2_ARATH
20	753	48.7	387	1	ADT2_MAIZE
21	752.5	48.6	318	1	ADT2_YEAST
22	752	48.6	386	1	ADT1_SOLTU
23	750	48.5	382	1	ADT1_SOLTU
24	749.5	48.4	305	1	ADT_ORYSA
25	747.5	48.3	381	1	ADT1_ARATH
26	744	48.1	331	1	ADT1_WHEAT
27	741.5	47.9	386	1	ADT2_SOLTU
28	737	47.6	331	1	ADT2_WHEAT
29	728	47.1	309	1	ADT1_YEAST
30	312.5	20.2	565	1	CMC2_CABEL
31	307	19.8	588	1	CMC2_CABEL
32	285	18.4	330	1	GDC_BOVIN
33	284	18.4	307	1	ODC2_YEAST

## ALIGNMENTS

34	278	18.0	325	1	UCP5_MOUSE
35	276.5	17.9	322	1	GDC_RAT
36	276.5	17.9	702	1	CMC1_CABEL
37	276	17.8	678	1	CMC1_HUMAN
38	274	17.7	325	1	UCP5_HUMAN
39	265.5	17.2	332	1	GDC_HUMAN
40	265	17.1	306	1	CMG5_MOUSE
41	261.5	16.9	675	1	CMC2_HUMAN
42	261	16.9	310	1	ODC1_YEAST
43	257.5	16.6	315	1	MPT_HUMAN
44	256	16.5	303	1	CM69_HUMAN
45	249.5	16.1	326	1	YEO8_SCHPO

092b2 mus musculus  
P16261 rattus norv  
O21153 caenorhabdi  
O75746 homo sapien  
O95258 homo sapien  
P16260 homo sapien  
O81103 mus musculus  
O91950 homo sapien  
O03028 saccharomyc  
Q9h2d1 homo sapien  
O8n8r3 homo sapien  
O13805 schizosacch

## RESULT 1

ADT2_HUMAN	STANDARD;	PRT;	298 AA.
AC	P05141; O43350;		
DT	13-AUG-1987 (Rel. 05, Created)		
DT	01-OCT-1994 (Rel. 30, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)		
DE	(Adenine nucleotide translocator 2) (ANT 2).		
GN	SLC25A5 OR ANT2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Mammalia; Primates; Carnivora; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Placenta;		
RX	MEDLINE=90375457; PubMed=2168878;		
RT	Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Murrel J.;		
RT	"The human fibroblast adenine nucleotide translocator gene. Molecular		
RT	cloning and sequence."		
RT	J. Biol. Chem. 265:16060-16063 (1990).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=8716056; PubMed=3031073;		
RT	Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.;		
RT	"Molecular cloning of a cDNA for a human ADP/ATP carrier which is		
RT	growth-regulated."		
RT	J. Biol. Chem. 262:4355-4358 (1987).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Chen C.N., Su Y., Baydayan P., Siruno A., Nagaraja R.;		
RA	Mazarella R.A., Schlessinger D., Chen B.Y.;		
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RA	Becker M., Graves T., Ozersky P.;		
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE OF 47-298 FROM N.A.		
RC	TISSUE=Liver;		
RX	MEDLINE=88124845; PubMed=2829183;		
RT	Houldsworth J., Attardi G.;		
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA		
RT	level in adult human liver."		
RT	Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).		
RL	FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE		
CC	MITOCHONDRIAL INNER MEMBRANE.		
CC	-1- SUBUNIT: Homodimer.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial		
CC	inner membrane.		
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.		
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.		
CC	-----		
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----  
 DR EMBL; M57424; AAA51797.1; -  
 DR EMBL; J02683; AAA55579.1; -  
 DR EMBL; L78810; AAB39266.1; -  
 DR EMBL; AC004000; AAB96347.1; -  
 DR EMBL; J03591; AAA36749.1; -  
 DR F1R; A29132; A29132.  
 DR Genew; HGNC:10991; SLC25A5.  
 DR MIM; 300150; -  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0015207; P: adenine transporter activity; TAS.  
 DR GO; GO:0006832; P: small molecule transport; TAS.  
 DR InterPro; IPR002067; Mtc carrier.  
 DR InterPro; IPR002030; Mtc uncoupling.  
 DR Pfam; PF00153; mltc carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 FT CONFLICT 6 6 V -> L (IN REF. 2).  
 FT CONFLICT 66 66 G -> E (IN REF. 2).  
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).  
 FT CONFLICT 162 162 V -> G (IN REF. 5).  
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 99.4%; Score 1537; DB 1; Length 298;  
 Best Local Similarity 99.3%; Pred. No. 8,9e-128;

Matches 296; Conservative 1; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 MTDALSPKDFLAGGVAALSKTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
 DB 1 MTDAAVSFAKDFLAGGVAALSKTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
 QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFWRYFAGNLASG 120  
 DB 61 IPKEQGVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYVPLDFAFRLADVGKAGAREFRGLDCLVKYIKSGIKGLYGFNVNS 180  
 DB 121 GAAGATSLCFYVPLDFAFRLADVGKAGAREFRGLDCLVKYIKSGIKGLYGFNVNS 180  
 QY 181 VGGIITRAAYFGIYDTAKGMLPDPKNTHTIYSMMIAQTVAVAGLTSPPTVRRMM 240  
 DB 181 VGGIITRAAYFGIYDTAKGMLPDPKNTHTIYSMMIAQTVAVAGLTSPPTVRRMM 240  
 QY 241 QSGRGKTDIMYGTLDCKWKIARDEGKAFKAGANSNVLRGGAFFVLVYDEIKKYYT 298  
 DB 241 QSGRGKTDIMYGTLDCKWKIARDEGKAFKAGANSNVLRGGAFFVLVYDEIKKYYT 298

RESULT 2  
 ADT2 RAT STANDARD; PRT; 298 AA.  
 ID ADT2 RAT  
 AC 009073;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 GN (Adenine nucleotide translocator 2) (ANT 2).  
 OS SLC25A5 OR ANT2.  
 CC Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RX STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=94002161; PubMed=8399300;  
 RA Shinozaki Y., Kanada M., Yamazaki N., Terada H.;  
 RT "Isolation and characterization of cDNA clones and a genomic clone  
 RT encoding rat mitochondrial adenine nucleotide translocator."  
 RL Biochim. Biophys. Acta 1152:192-196 (1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND  
 CC SKELETAL MUSCLE.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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DR EMBL; D12771; BAA02338.1; -  
 DR InterPro; IPR002067; Mtc carrier.  
 DR InterPro; IPR002030; Mtc uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mltc carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987BE935 CRC64;

Query Match 98.6%; Score 1525; DB 1; Length 298;  
 Best Local Similarity 98.3%; Pred. No. 1e-126;  
 Matches 293; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDALSPKDFLAGGVAALSKTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
 DB 1 MTDAAVSFAKDFLAGGVAALSKTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
 QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFWRYFAGNLASG 120  
 DB 61 IPKEQGVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYVPLDFAFRLADVGKAGAREFRGLDCLVKYIKSGIKGLYGFNVNS 180  
 DB 121 GAAGATSLCFYVPLDFAFRLADVGKAGAREFRGLDCLVKYIKSGIKGLYGFNVNS 180  
 QY 181 VGGIITRAAYFGIYDTAKGMLPDPKNTHTIYSMMIAQTVAVAGLTSPPTVRRMM 240  
 DB 181 VGGIITRAAYFGIYDTAKGMLPDPKNTHTIYSMMIAQTVAVAGLTSPPTVRRMM 240

DB 181 VGGIIYRAAFYGIYDIAKMLPDPKXTHIFISWMIQSVTAAGLTSPEDTVRRMM 240

QY 241 OSGRKTDIMTGTLDCKRKIARDGSKAFKAGMSNLRMGGAFLVLYDEIKKT 298

DB 241 OSGRKTDIMTGTLDCKRKIARDGSKAFKAGMSNLRMGGAFLVLYDEIKKT 298

RESULT 3

ID ADT2\_MOUSE STANDARD; PRT; 298 AA.

AC P51881; Q61311;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)

DB (Adenine nucleotide translocator 2) (ANT 2).

GN SLC25A5 OR ANT2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=97059403; PubMed=8903724;

RA Ellison J.W., Li X., Francke U., Shapiro L.J.;

RT "Rapid evolution of human pseudautosomal genes and their mouse homologs.";

RL Mamm. Genome 7:25-30(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RA Sheldon J.G.;

RL Thesis (1995), University of Cambridge, U.K.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/Sv;

RA Costet P., Laplace C.;

RT Submitted (FEB-1993) to the EMBL/genbank/DBJ databases.

RN [4]

RP REVISIONS.

RA Laplace C.;

RL Submitted (FEB-1997) to the EMBL/genbank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=20432087; PubMed=10974536;

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;

RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";

RL Gene 254:57-66(2000).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC -----

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CC -----

CC EMBL; U27316; AAC52838.1; -

CC EMBL; U10404; AAA19009.1; -

CC EMBL; X70847; CAAS0196.1; -

CC EMBL; AF240003; AAF64471.1; -

CC MGD; MGI:1353496; SLC25A5.

CC InterPro; IPR002067; Mlt\_carrier.

CC InterPro; IPR002030; Mlt\_uncoupling.

DR InterPro; IPR001993; Mitoch carrier.

DR Pfam; PF00153; mito\_carr; 3

DR PRINTS; PRO0926; MITOCARRIER.

DR PRINTS; PRO0784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH\_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multi-gene family.

FT TRANSMEM 12 29 1 (POTENTIAL).

FT TRANSMEM 73 91 2 (POTENTIAL).

FT TRANSMEM 117 134 3 (POTENTIAL).

FT TRANSMEM 176 195 4 (POTENTIAL).

FT TRANSMEM 214 231 5 (POTENTIAL).

FT TRANSMEM 273 291 6 (POTENTIAL).

FT REPEAT 1 111 1.

FT REPEAT 112 208 2.

FT REPEAT 209 298 3.

SO SEQUENCE 298 AA; 32931 MW; 0798B04B987FE820 CRC64;

Query Match 98.2%; Score 1519; DB 1; Length 298;

Best Local Similarity 98.0%; Pred. No. 3.4e-126;

Matches 292; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTDAAISFADKFLAGVAAAIKTAIVAPIERVKLLQVQHASKOITADKOYKGIIDCVR 60

DB 1 MTDAAISFADKFLAGVAAAIKTAIVAPIERVKLLQVQHASKOITADKOYKGIIDCVR 60

QY 61 IPKEQVLSTFRGMLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNTASG 120

DB 61 IPKEQVLSTFRGMLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNTASG 120

QY 121 GAAGATSLCFYPLDPAFTRIAADVAGKAGAREBRGJGDCIVLYKSGIKGLQGFVNS 180

DB 121 GAAGATSLCFYPLDPAFTRIAADVAGKAGAREBRGJGDCIVLYKSGIKGLQGFVNS 180

QY 121 VGGIIYRAAFYGIYDIAKMLPDPKXTHIFISWMIQSVTAAGLTSPEDTVRRMM 240

DB 181 VGGIIYRAAFYGIYDIAKMLPDPKXTHIFISWMIQSVTAAGLTSPEDTVRRMM 240

QY 241 OSGRKTDIMTGTLDCKRKIARDGSKAFKAGMSNLRMGGAFLVLYDEIKKT 298

DB 241 OSGRKTDIMTGTLDCKRKIARDGSKAFKAGMSNLRMGGAFLVLYDEIKKT 298

RESULT 4

ID ADT3\_BOVIN STANDARD; PRT; 298 AA.

AC P32007;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE ADP,ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).

GN SLC25A6 OR ANT3.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89228093; PubMed=2540808;

RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;

RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";

RL Biochemistry 28:866-873(1989).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC -----

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CC EMBL; M24103; AAA30769.1; -  
 CC PIR; B43646; B43646.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_car\_3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUOCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 2 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6E8DE4061 CRC64;

Query Match 94.2%; Score 1458; DB 1; Length 298;  
 Beel Local Similarity 92.9%; Pred. No. 7.7e-121;  
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAIAIKTAAPAPERVKLLVOHASKQOTADKQVGIIDCYR 60  
 DB 1 MTEQAIISPKDPLAGVAIAIAIKTAAPAPERVKLLVOHASKQOTADKQVGIIDCYR 60  
 QY 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFDKTKQIPLGVDNRTQFWRYFAGNLASG 120  
 DB 61 IPKEQGVLSFWKGNLANVIRYPTQALNFAFDKTKQIPLGVDNRTQFWRYFAGNLASG 120  
 QY 121 GAAGTSLCTFYPPDLPARTRLADYKAGAEFFGLDCLVYIKYSIDGKILYGGFNVS 180  
 DB 121 GAAGTSLCTFYPPDLPARTRLADYKAGAEFFGLDCLVYIKYSIDGKILYGGFNVS 180  
 QY 121 GAAGTSLCTFYPPDLPARTRLADYKAGAEFFGLDCLVYIKYSIDGKILYGGFNVS 180  
 DB 121 GAAGTSLCTFYPPDLPARTRLADYKAGAEFFGLDCLVYIKYSIDGKILYGGFNVS 180  
 QY 181 VGGIIYRAAYRGIDTAKGMLPDPKNTHTVSNMIAQTVAVAGLTSYPTVARRMM 240  
 DB 181 VGGIIYRAAYRGIDTAKGMLPDPKNTHTVSNMIAQTVAVAGLTSYPTVARRMM 240  
 QY 241 QSGRGKTDIMYTGTLDCWRKIKARDEGKAFKFGANSVLRGNGAFVLYLXDEIKK 296  
 DB 241 QSGRGKTDIMYTGTLDCWRKIKARDEGKAFKFGANSVLRGNGAFVLYLXDEIKK 296  
 QY 241 QSGRGKTDIMYTGTLDCWRKIKARDEGKAFKFGANSVLRGNGAFVLYLXDEIKK 296  
 DB 241 QSGRGKTDIMYTGTLDCWRKIKARDEGKAFKFGANSVLRGNGAFVLYLXDEIKK 296

RESULT 5  
 ADT3 HUMAN STANDARD; PRT; 298 AA.  
 ID ADT3\_HUMAN  
 AC P12336; Q96C49; Rel. 12; Created  
 DT 01-OCT-1989 (Rel. 12; Last sequence update)  
 DT 01-NOV-1999 (Rel. 16; Last annotation update)  
 DT 15-SEP-2003 (Rel. 42; Last annotation update)  
 DE ADP carrier protein, liver isoform T2 (ADP/ATP translocase 3)  
 DE (Adenine nucleotide translocator 3) (ANT 3).  
 GN SLG25A6 OR ANT3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89236396; PubMed=2541251;  
 RA Cozens A.L., Runswick M.J., Walker J.E.;

RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
 RT ADP/ATP translocase.";  
 RT J. Mol. Biol. 206:261-280 (1989).

RP SEQUENCE FROM N.A.  
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
 RA Margolin J.P.,  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RP TISSUE=Brain; Cervix, Eye, and Lung;  
 RX MEDLINE=2238257; PubMed=12477932;

RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshitsuki S., Carrinci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska J., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RT [4]

RP SEQUENCE OF 36-298 FROM N.A.

RC TISSUE=Liver;  
 RX MEDLINE=88124845; PubMed=2829183;

RA Houldsworth J., Actardi G.,  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 RT level in adult human liver.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL; J03592; AAA36750.1; -  
 CC EMBL; AY007135; AAG01998.1; -  
 CC EMBL; BC007295; AAH07295.1; -  
 CC EMBL; BC007850; AAH07850.1; -  
 CC EMBL; BC008737; AAH08737.1; -  
 CC EMBL; BC008935; AAH08935.1; -  
 CC EMBL; BC014775; AAH14775.1; -  
 CC PIR; S03894; S03894.  
 DR Gene; HGNC:10992; SLG25A6.  
 DR MIM; 300151; -  
 DR MIM; 403000; -  
 DR GO; GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.  
 DR GO; GO:0005471; F:ATP/ADP antiporter activity; TAS.  
 DR GO; GO:0006854; P:ATP/ADP exchange; TAS.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.



DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PRO0926; MITOCARRIER.  
 DR PRINTS; PRO0784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 MW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 100 1.  
 FT REPEAT 101 208 2.  
 FT REPEAT 209 298 3.  
 FT REPEAT 105 108 4.  
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAHL14775).  
 FT SEQUENCE 298 AA; 32866 MW; 1853489F0B49672P CRC64;  
 Query Match 94.0%; Score 1454; DB 1; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 1.7e-120;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MTDAAISPAKDFLAGGVAASIKTAAPVIEBVKLLQVQHASKQITTDKQYKGIIDCVR 60  
 DB 1 MTEQASIPAKDFLAGGVAASIKTAAPVIEBVKLLQVQHASKQITTDKQYKGIIDCVR 60  
 QY 61 IPKQEVLSFWRGMLANVIRFPFOALNPAKDKKQIFLGVDKRTFPRNFRANLASC 120  
 DB 61 IPKQGVLSFWRGMLANVIRFPFOALNPAKDKKQIFLGVDKRTFPRNFRANLASC 120  
 QY 121 GAAGATSLCFYPLDPAFTRIAADYKAGARBPFGDGLVKIKYSGDIGLQGFVNS 180  
 DB 121 GAAGATSLCFYPLDPAFTRIAADYKAGARBPFGDGLVKIKYSGDIGLQGFVNS 180  
 QY 181 VQGIIVYAAVFGYIDAKGMLPDKNTHIVISWMLAQTVAVAGLTSYPPDYRRMM 240  
 DB 181 VQGIIVYAAVFGYIDAKGMLPDKNTHIVISWMLAQTVAVAGLTSYPPDYRRMM 240  
 QY 241 QSGRKGIDIMYTGTLDCRKRIARDEGGAFFKGAWSNVLKMGAFVLYLDEIK 296  
 DB 241 QSGRKGIDIMYTGTLDCRKRIARDEGGAFFKGAWSNVLKMGAFVLYLDEIK 296  
 RESULT 6  
 ADT1\_MOUSE STANDARD; PRT; 298 AA.  
 AC P48962; O62164;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DB ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1) (MANC1).  
 GN SLG25A4 OR ANT1 OR ANCL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA MEDLINE=97059403; PubMed=8903724;  
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.,  
 RT "Rapid evolution of human pseudautosomal genes and their mouse  
 RL homologs";  
 RL Mamm. Genome 7:25-30 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Muscle;  
 RA Laplace C., Costet P.,  
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;  
 RT "Expression and sequence analysis of the mouse adenine nucleotide  
 RL translocase 1 and 2 genes";  
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin J., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Kana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,  
 RA Binkley K.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RL human and mouse cDNA sequences";  
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -1 FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1 SUBUNIT: Homodimer.  
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1 SIMILARITY: Belongs to the mitochondrial carrier family.  
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 CC -----  
 CC EMBL; U27315; AAC52837.1; -  
 CC EMBL; X74510; CAAS2616.1; -  
 CC EMBL; AF240002; AAF64470.1; -  
 CC EMBL; BC003791; AAH03791.1; -  
 CC EMBL; BC026925; AAH26925.1; -  
 CC PIR; S37210; S37210.  
 CC MGI; MGI:1353495; Slc25a4.  
 DR InterPro; IPR002067; Mlt carrier.  
 DR InterPro; IPR002030; Mlt uncoupling.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PRO0926; MITOCARRIER.  
 DR PRINTS; PRO0784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 MW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 110 1.  
 FT REPEAT 111 208 2.  
 FT REPEAT 209 298 3.  
 FT CONFLICT 136 136 F -> L (IN REF. 1).  
 FT SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;  
 Query Match 91.6%; Score 1417; DB 1; Length 298;

Best Local Similarity 89.6%, Pred. No. 3.1e-117,  
Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDFLAGGVAALISKTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
DB 1 MGDAALSLKDFLAGGIAAASKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRR 60  
QY 61 IPKEQEVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
DB 61 IPKEQGFISFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
QY 121 GAAGATSLCFYVPLDPAFTRILADVKGAGAREFRGLDCLVKIKYSGDGLKGLYQGFVS 180  
DB 121 GAAGATSLCFYVPLDPAFTRILADVKGAGAREFRGLDCLVKIKYSGDGLKGLYQGFVS 180  
QY 181 VGGIIITRAAYFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAAGLTSPEDTVARRMM 240  
DB 181 VGGIIITRAAYFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAAGLTSPEDTVARRMM 240  
QY 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFPKGANSVLRMGAFVLVYDEIKKY 297  
DB 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFPKGANSVLRMGAFVLVYDEIKKY 297

RESULT 7  
ADT1 RAT STANDARD; PRT; 298 AA.

AC Q05962;  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
GN SLC25A4 OR ANT1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94002161; PubMed=8399300;  
RA Shinohara Y., Kanada M., Yamazaki N., Terada H.;  
RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator";  
RL Biochim. Biophys. Acta 1152:192-196(1993).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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CC -----  
DR EMBL; X61667; CA443842.1; -;  
DR EMBL; D12770; BAA02237.1; -;  
DR PIR; I60173; I60173.  
DR InterPro; IPR002067; Mit\_carrier.  
DR InterPro; IPR002030; Mit\_uncoupling.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mito\_carr; 3-  
DR PRINTS; PR00926; MITOCARRIER.  
DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multi-gene family.  
FT TRANSMEM 12 29 1 (POTENTIAL).  
FT TRANSMEM 73 91 2 (POTENTIAL).  
FT TRANSMEM 117 134 3 (POTENTIAL).  
FT TRANSMEM 176 195 4 (POTENTIAL).  
FT TRANSMEM 214 231 5 (POTENTIAL).  
FT TRANSMEM 273 291 6 (POTENTIAL).  
FT REPEAT 1 110 1.  
FT REPEAT 111 208 2.  
FT REPEAT 209 298 3.  
SQ SEQUENCE 298 AA; 3298 MM; 66704FF78C6B320 CRC64;  
Query Match 91.6%, Score 1417; DB 1; Length 298;  
Best Local Similarity 89.6%, Pred. No. 3.1e-117,  
Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDFLAGGVAALISKTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60  
DB 1 MGDAALSLKDFLAGGIAAASKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRR 60  
QY 61 IPKEQEVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
DB 61 IPKEQGFISFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120  
QY 121 GAAGATSLCFYVPLDPAFTRILADVKGAGAREFRGLDCLVKIKYSGDGLKGLYQGFVS 180  
DB 121 GAAGATSLCFYVPLDPAFTRILADVKGAGAREFRGLDCLVKIKYSGDGLKGLYQGFVS 180  
QY 181 VGGIIITRAAYFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAAGLTSPEDTVARRMM 240  
DB 181 VGGIIITRAAYFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAAGLTSPEDTVARRMM 240  
QY 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFPKGANSVLRMGAFVLVYDEIKKY 297  
DB 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFPKGANSVLRMGAFVLVYDEIKKY 297

RESULT 8  
ADT1 BOVIN STANDARD; PRT; 297 AA.

AC P02722;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
GN SLC25A4 OR ANT1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82188267; PubMed=2540808;  
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.B.;  
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues";  
RL Biochemistry 28:866-873(1989).  
CC -----  
DR EMBL; X61667; CA443842.1; -;  
DR EMBL; D12770; BAA02237.1; -;  
DR PIR; I60173; I60173.  
DR InterPro; IPR002067; Mit\_carrier.  
DR InterPro; IPR002030; Mit\_uncoupling.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mito\_carr; 3-  
DR PRINTS; PR00926; MITOCARRIER.  
DR PRINTS; PR00784; MTUNCOUPLING.

RT an unusually short 3'-noncoding sequence.";  
 RL Biochem. Biophys. Res. Commun. 138:850-857(1986).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, M13783; AAA0363.1; -;  
 DR EMBL, M24102; AAA0768.1; -;  
 DR PIR, A46646; XMB0.  
 DR InterPro, IPR002067; Mit\_carrier.  
 DR InterPro, IPR002030; Mit\_uncoupling.  
 DR InterPro, IPR001993; Mitoch\_carrier.  
 DR Pfam, PF00153; mito\_car; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE, PS00215; MITOCH\_CARRIER; 3.  
 DR KMW; Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family; Methylation.  
 FT MOD\_RES 0 1  
 FT INIT MET 0  
 FT MOD\_RES 1 1  
 FT TRANSMEM 11 51  
 FT TRANSMEM 11 28  
 FT TRANSMEM 72 90  
 FT TRANSMEM 116 133  
 FT TRANSMEM 175 194  
 FT TRANSMEM 213 230  
 FT TRANSMEM 272 290  
 FT REPEAT 1 110  
 FT REPEAT 111 207  
 FT REPEAT 208 297  
 FT REPEAT 297 3  
 SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;  
 Query Match 91.4%; Score 1414; DB 1; Length 297;  
 Best Local Similarity 89.9%; Pred. No. 5,6e-117;  
 Matches 266; Conservative 16; Mismatches 14; Indels 0; Gaps 0;  
 Oy 2 TDAALSPADFLAGVAAAIKTAAPVPIERVLTALQVGHASKQITADKQYGIIDCVRI 61  
 Db 1 SDALSPFKDPLAGVAAAIKTAAPVPIERVLTALQVGHASKQISAEKQYGIIDCVRI 60  
 Oy 62 PKQEVLSFWRGNLNVIRYPTQALNFAFDKQYQIFLGGVDKRTQFWRYPAGNLASGG 121  
 Db 61 PKQGVLSFWRGNLNVIRYPTQALNFAFDKQYQIFLGGVDKRTQFWRYPAGNLASGG 120  
 Oy 122 AAGATSLCFVYPLDPARTLADVKGAGAEFRFGLGCLYKITYSDGIGKLYGCFNVS 181  
 Db 121 AAGATSLCFVYPLDPARTLADVKGAGAEFRFGLGCLYKITYSDGIGKLYGCFNVS 180  
 Oy 182 QGIIIRAYRAGIYDTAKGMLPDPNGTHIVISMMIAQVTVAGLTSYPPPTVRBRMMQ 241  
 Db 181 QGIIIRAYRAGIYDTAKGMLPDPNGTHIVISMMIAQVTVAGLTSYPPPTVRBRMMQ 240  
 Oy 242 SGRKGTIDIMYTGTDLCWRKIARDEGKAFPKGAWSNVLRNGGAFVLVLYDEIKKY 297  
 Db 241 SGRKGTIDIMYTGTDLCWRKIARDEGKAFPKGAWSNVLRNGGAFVLVLYDEIKKY 296

DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP  
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
 GN SLG2544 OR ANT1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OK NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89236396; PubMed=2541251;  
 RA Cozens A.L., Runswick M.J., Walker J.E.;  
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
 RT ADP/ATP translocase.";  
 RL J. Mol. Biol. 206:261-280(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89340499; PubMed=2547778;  
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,  
 RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;  
 RT "A human muscle adenine nucleotide translocator gene has four exons,  
 RT is located on chromosome 4, and is differentially expressed.";  
 RL J. Biol. Chem. 264:13998-14004(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88041149; PubMed=2823266;  
 RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;  
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack  
 RT of a leader peptide, divergence from a fibroblast translocator cDNA,  
 RT and coevolution with mitochondrial DNA genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=23388257; PubMed=12477932;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stedler M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,  
 RA Rana S.S., Lequellano N.A., Peters G.J., Adarnson R.D., Mullany S.J.,  
 RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Abbey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska J., Smalins D.E.,  
 RA Scherch A., Schein J.R., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP SEQUENCE OF 1-37 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88124845; PubMed=2829183;  
 RA Houldsworth J., Atterdall G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 RT level in adult human liver.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
 RN [6]  
 RP VARIANTS PRO-114 AND MET-289.  
 RX MEDLINE=20385067; PubMed=10926541;  
 RA Kaukonen J., Uuseliu J.K., Tiranli V., Kyttala A., Zeviani M.,  
 RA Comi G.P., Keranen J., Peltomen L., Suomalainen A.;  
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";  
 RL Science 289:782-785(2000).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- DISEASE: Defects in SLIC25A4 are a cause of autosomal dominant  
 CC progressive external ophthalmoplegia with various mitochondrial  
 CC DNA deletions (PEO). Patients with PEO have mitochondrial  
 CC myopathy, progressive external ophthalmoplegia, and other  
 CC abnormalities associated with multiple different deletions of  
 CC mitochondrial DNA.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC -----  
 DR EMBL: J02366; AAA61223.1; -  
 DR EMBL: J03593; AAA36751.1; -  
 DR EMBL: J04982; AAA51736.1; -  
 DR EMBL: BC008664; AA08664.1; -  
 DR PIR: A44778; A44778.  
 DR Genew: HGNC:10990; SLIC25A4.  
 DR MIM: 103220; -  
 DR MIM: 157640; -  
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO: GO:0005739; C: mitochondrion; TAS.  
 DR GO: GO:0015207; P: adenine transporter activity; TAS.  
 DR GO: GO:0006091; P: energy pathways; TAS.  
 DR GO: GO:0000002; P: mitochondrial genome maintenance; TAS.  
 DR GO: GO:0006833; P: small molecule transport; TAS.  
 DR InterPro: IPR002067; Mtc\_carrier.  
 DR InterPro: IPR002030; Mtc\_uncoupling.  
 DR InterPro: IPR001993; Mito\_carrier.  
 DR Pfam: PF00153; mto\_carrier\_3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PRINTS: PR00784; MTINCouPLING.  
 DR PROSITE: PS00215; MITOCH\_CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family; Disease mutation.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 110 1.  
 FT REPEAT 111 208 2.  
 FT REPEAT 209 298 3.  
 FT VARIANT 114 114 A->P (IN PEO).  
 FT VARIANT 289 289 /FTID=VAR\_012111.  
 FT VARIANT 289 289 V->M (IN PEO).  
 FT CONFLICT 16 16 G->A (IN REF. 3).  
 FT CONFLICT 147 149 GCA->A (IN REF. 3).  
 FT CONFLICT 227 227 V->L (IN REF. 3).  
 SO SEQUENCE .298 AA; 33064 MW; 59F0D9AEC4E7FEBB CRC64;  
 Query Match 91.3%; Score 1413; DB 1; Length 298;  
 Best Local Similarity 89.2%; Pred. No. 6.9e-117;  
 Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 121 GAAGATSLCFYVPLDFAFTRLAADVAGAGAEERERGLDCLVKIKYSDGINGLYGFRVNS 180  
 DB GAAGATSLCFYVPLDFAFTRLAADVAGAGAEERERGLDCLVKIKYSDGINGLYGFRVNS 180  
 QY 161 VGGIITVYAAAFPGIYDTAKGMLPPPKNTHIYISNMIAQTVANVGLTSPYPTDTRRRMM 240  
 DB 161 VGGIITVYAAAFPGIYDTAKGMLPPPKNTHIYISNMIAQTVANVGLTSPYPTDTRRRMM 240  
 QY 241 QSGRKGTDMYTGTLDCRKRJARDEGGAFFKGAAMSNVLRMGAFVVLVDEIKKY 297  
 DB 241 QSGRKGTDMYTGTLDCRKRJARDEGGAFFKGAAMSNVLRMGAFVVLVDEIKKY 297  
 RESULT 10  
 ADT\_DROME STANDARD; PRT; 299 AA.  
 AC Q26365; P91614; Q26254; Q95S30; Q9VZ70;  
 DT 15-OUL-1998 (Rel. 36, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
 DE translocator) (ANT) (Stress sensitive B protein).  
 GN SEEB OR A/A-T OR CG16944.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92389367; PubMed=1387687;  
 RA Louvi A., Tsililou S.G.;  
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila  
 RT melanogaster shows a high degree of similarity with the mammalian  
 RT ADP/ATP translocases".  
 RL J. Mol. Evol. 35:44-50(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94350065; PubMed=7520869;  
 RA Hutter P., Karch F.;  
 RT "Molecular analysis of a candidate gene for the reproductive  
 RT isolation between sibling species of Drosophila".  
 RL Experientia 50:749-762(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Oregon-R;  
 RA Zhang Y.O., Davis A.W., Roote J., Herrmann S., Ashburner M.;  
 RL Submitted (JMN-1997) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hopkins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,  
 RA Botkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,  
 RA Butcher K.C., Butnam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalish J., Karpen G.H., Ke Z., Kemtson J.A., Ketchum K.A.,

Query Match	81.0%	Score 1253.5	DB 1	Length 299
Best Local Similarity	81.2%	Pred. No. 7.1e-103		
Matches 237	Conservative 21	Mismatch 33	Indels 1	Gaps 1
Qy	5	ALSPADFLAGVAAAIKSTKVAIPERVKLLQVQHASKOITPAKQYKGIIDCVRIPEK	64	
Db	7	AVGVVDQPAAGGISAASKRAVAIERVKLLQVQHSKQISPKQYKGMWDCIRIPKE	66	
Qy	65	QEVLSFMRGNLANIYRYFTQALNFAFKDKYKQIFLGVDKRTQPMRYPAGNLASGGAAG	124	
Db	67	QGFSSFMKGNLANIYRYFTQALNFAFKDKYKQIFLGVDKRTQPMRYPAGNLASGGAAG	126	
Qy	125	ATSLCFYYPIDPATRILAADVGRKAGAREPRLGDCLVKIKSGIKGLYQGFVNSVQGI	184	
Db	127	ATSLCFYYPIDPATRILAADVGRKAGAREPRLGDCLVKIKSGIKGLYQGFVNSVQGI	185	
Qy	185	IYYBAAFVGIYDTKAGMLPDPKNTPIYISNMIAQTVVAAGLTSYPPPTVRRMMOSGR	244	
Db	186	IYYBAAFVGIYDTKAGMLPDPKNTPIYISNMIAQTVVAAGLTSYPPPTVRRMMOSGR	245	
Qy	245	KGIDIMYTGTLDCWRKTLARDEGKAFPKGASMSVLRGMAFVLYLDEIKK	296	
Db	246	KATEVIYKNTLHCWATLAKQEGTAFPKGAFSNLTIRGTGAFVLYLDEIKK	297	
RESULT 11				
ID	ADT ANOGA	STANDARD	PRT	301 AA.
AC	Q27238			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	01-NOV-1997	(Rel. 35, Last annotation update)		
DE	ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT)			
OS	Anopheles gambiae (African malaria mosquito).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.			
OX	NCBI_TaxID=7165;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=G3.			
FX	MEDLINE=94348635; PubMed=8069414;			
RA	Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins P.H.;			
RT	"A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae."			
RL	Insect Mol. Biol. 3:35-40(1994).			
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.			
CC	-1- SUBUNIT: Homodimer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.			
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.			
CC	-----			
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CC	-----			
DR	EMBL, L11618; AAB04104.1; -			
DR	EMBL, L11617; AAB04105.1; -			
DR	InterPro; IPR002067; Mlt_carrier.			
DR	InterPro; IPR001993; Mitoch_carrier.			
DR	Pfam; PF00153; mltc_carr; 3.			
DR	PRINTS; PR00926; MITOCHARRIER.			
DR	PROSITE; PS00215; MITOCH_CARRIER_3.			
KT	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.			
FM	TRANSMEM 14 31 1 (POTENTIAL).			
FT	TRANSMEM 75 93 2 (POTENTIAL).			
FT	TRANSMEM 119 136 3 (POTENTIAL).			

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FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 216 233 5 (POTENTIAL).
FT TRANSMEM 275 293 6 (POTENTIAL).
SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8D08B CRC64;

Query Match
Best Local Similarity 76.9%; Score 1190; DB 1; Length 301;
Matches 227; Conservative 18; Mismatches 43; Indels 0; Gaps 0;

QY 8 FAKDLIAGGVAIAIKTAVAPIERVYLLIQVHASKQITADKQYKGIIDCVRIKPEOE 67
DB 10 FAKDLIAGGVAIAIKTAVAPIERVYLLIQVHASKQITADKQYKGIIDCVRIKPEOE 69

QY 68 LSEFWGNLANVIRYPTQALNFAFKQKQIFLGVDKRTQWRYPAGNLASGGAAGTS 127
DB 70 GAFWNGNLANVIRYPTQALNFAFKQKQIFLGVDKRTQWRYPAGNLASGGAAGTS 129

QY 128 LCFVYPLDPARTRLADVGKAGABERFGLGDCIKYKSDGIRKLYOGFNVSVGGIIY 187
DB 130 LCFVYPLDPARTRLADVGKAGABERFGLGDCIKYKSDGIRKLYOGFNVSVGGIIY 189

QY 188 RAAVGIYDTAKGMLPDPKNTHTIVISWIAQTVAAGLTSYPTDVRMMQSGRKGT 247
DB 190 RAAVGCCTDTAKGMLPDPKNTHTIVISWIAQTVAAGLTSYPTDVRMMQSGRKGT 249

QY 248 DIMYTGTLDCWRKIARDGKAPFKGAMSNVLRGKGAFVLYYDEIK 295
DB 250 EVMYKNTLDCWVKIKQSGSGAFPFKGFNSVLRGTGALVLYYDEIK 297

RESULT 12
ADT_CHUNK STANDARD; PRT; 339 AA.
AC P31692;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
OS translocator) (ANT).
OS Chlorella kesselii.
OS Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_Taxid=3074;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084708; PubMed=1748677;
RA Hilgarch C., Sauer N., Tanner W.;
RT "Glucose increases the expression of the ATP/ADP translocator and the
RT glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";
RL J. Biol. Chem. 266:24044-24047(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC -----
CC EMBL, M76669; AAA33027.1; -
CC PIR, A41677; A41677.
CC InterPro, IPR002067; Mlt carrier.
CC InterPro, IPR001993; MitoCh carrier.
CC Pfam, PF00153; mltc_carr; 3_
CC PRINTS, PR000926; MITOCARRIER.
CC PROSITE, PS00215; MITOCH_CARRIER; 3.

```

```

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 45 62 1 (POTENTIAL).
FT TRANSMEM 108 126 2 (POTENTIAL).
FT TRANSMEM 151 168 3 (POTENTIAL).
FT TRANSMEM 209 228 4 (POTENTIAL).
FT TRANSMEM 248 265 5 (POTENTIAL).
FT TRANSMEM 304 322 6 (POTENTIAL).
SQ SEQUENCE 339 AA; 36686 MW; 54779734A3B3942 CRC64;

Query Match
Best Local Similarity 62.6%; Score 968; DB 1; Length 339;
Matches 194; Conservative 29; Mismatches 64; Indels 8; Gaps 5;

QY 6 LSPFADLAGGVAIAIKTAVAPIERVYLLIQVHASKQITADK-QYKGIIDCVRIK 63
DB 39 MAFVYDLIAGGTAGIAIKTAVAPIERVYLLIQVHASKQITADK-QYKGIIDCVRIK 98

QY 64 BOEVLSPFNGNLANVIRYPTQALNFAFKQKQIFLGVDKRTQWRYPAGNLASGGA 123
DB 99 BOGVASFWGNLANVIRYPTQALNFAFKQKQIFLGVDKRTQWRYPAGNLASGGA 157

QY 124 GATSLCFVYPLDPARTRLADVGKAGABERFGLGDCIKYKSDGIRKLYOGFNVSVGG 183
DB 158 GAGSLIYVPLDPARTRLADVG-SGKSRFTGLVDCISKYVKGSGPMALYQGFVSYQG 216

QY 184 IITRAVGIYDTAKGMLPDPKNTHTIVISWIAQTVAAGLTSYPTDVRMMQSGRKGT 242
DB 217 IIVVGAFFGLYDTAKGMLPDPKNTHTIVISWIAQTVAAGLTSYPTDVRMMQSGRKGT 276

QY 243 GRKGTDIMYTGTLDCWRKIARDGKAPFKGAMSNVLRGKGAFVLYYDEIK 297
DB 277 ---GGERQYNGITDCWRKIARDGKAPFKGAMSNVLRGKGAFVLYYDEIK 328

RESULT 13
ADT1_GOSHI STANDARD; PRT; 386 AA.
AC O22342;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein 1, mitochondrial precursor (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
DE GN ANTI.
OS Gossypium hirsutum (Upland cotton).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Malvales; Malvaceae; Malvaceae; Gossypium.
OX NCBI_Taxid=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Texas Marker 1; TISSUE=Fiber;
RA Shin H., Brown R.M. Jr.;
RT "Two cDNA sequences for the adenine nucleotide translocator, CANT1 and
RT CANT2, from cotton fibers (Gossypium hirsutum).";
RL (In) Plant Gene Register PER97-130.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, AF006489; AAB72047.1; -
CC PIR, T09709; T09709.
CC InterPro, IPR002067; Mlt carrier.
CC InterPro, IPR001993; MitoCh carrier.
CC Pfam, PF00153; mltc_carr; 3.

```



DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH CARRIER; 2.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Transmembrane; Multigene family.  
 FT TRANSIT 1 76 MITOCHONDRION (BY SIMILARITY).  
 FT CHAIN 1 386 ADP, ATP CARRIER PROTEIN 1.  
 FT TRANSMEM 90 107 1 (POTENTIAL).  
 FT TRANSMEM 152 170 2 (POTENTIAL).  
 FT TRANSMEM 195 212 3 (POTENTIAL).  
 FT TRANSMEM 256 275 4 (POTENTIAL).  
 FT TRANSMEM 295 312 5 (POTENTIAL).  
 FT TRANSMEM 351 369 6 (POTENTIAL).  
 SQ SEQUENCE 386 AA; A05F76C73FECDE6 CRC64;  
 Query Match 49.8%; Score 771; DB 1; Length 386;  
 Best Local Similarity 53.4%; Pred. No. 2.3e-60;  
 Matches 169; Conservative 35; Mismatches 79; Indels 22; Gaps 7;  
 QY 7 SPANDFLAGVAAAIKSTAVAPIERVKLLQVQ--HASKQTADKQYGIIDCVIRPKQ 65  
 DB 85 SPALDFLMGVSAAVSKTAAPRIEVRKLLIONQDMISGRLSERYKGIIDCFKRTTID 144  
 QY 66 EVLSFWRGNLANVIRYPTQALNFAFKDKYQIIFLGVDKRTQFWRYFAGNLAAGGA 125  
 DB 145 GFGSLMRGNLANVIRYPTQALNFAFKDKYQIIFLGVDKRTQFWRYFAGNLAAGGA 203  
 QY 126 TSLCVVYLDPAFRTIADV--VGKAGAREFRGLDCLVKYKSGIKGLYQGFVNSV 183  
 DB 204 SSLLEVYSLDPAFRTIADV--VGKAGAREFRGLDCLVKYKSGIKGLYQGFVNSV 263  
 QY 184 IIVYRAVFGIYDPAK-----GMLPDPKNTIIVISMTIAQTAVTAAGLTSYPTVRRM 238  
 DB 264 IIVYRAVFGIYDPAK-----GMLPDPKNTIIVISMTIAQTAVTAAGLTSYPTVRRM 319  
 QY 239 MMSGRKKTIDIMYTGTLDCWRKRIARDEGKAFKFGAMSNVLKMGAGFVLVYDEI--- 294  
 DB 320 MMSGRKKTIDIMYTGTLDCWRKRIARDEGKAFKFGAMSNVLKMGAGFVLVYDEI--- 376  
 QY 295 --KKY 297  
 DB 377 FGKXY 381  
 RESULT 14  
 ADT\_SCHPO STANDARD; PRT; 322 AA.  
 ID ADT\_SCHPO  
 AC Q09188;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ADP, ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).  
 DE ANCI OR SPBC530.10C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 CC Schizosaccharomycetes; Schizosaccharomycetaceae;  
 CC Schizosaccharomycetes.  
 OC Schizosaccharomycetes.  
 NCBI TaxID=4896;  
 RX MEDLINE=96257204; PubMed=8675018;  
 RX MEDLINE=96257204; PubMed=8675018;  
 RA Courzin N., Trezeguet V., Sauk A.L., Lauguin G.J.M.;  
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomycetes pombe by functional complementation in Saccharomyces cerevisiae."  
 RL Gene 171:113-117(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RC MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris P., Hidalgo J., Hodgson G., Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moulé S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Voicikert G., Aert R., Robben J., Grymopiez B., Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer B., Moesli D., Hilbert H., Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Medler H., Wandt R., Punnelle B., Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S., Gallibert P., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Usery D., Bartell B.G., Nurse P.;  
 RA "The genome sequence of Schizosaccharomycetes pombe."  
 RL Nature 415:871-880(2002).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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 CC EMBL; Z49974; CA90275.1; -  
 CC EMBL; AL023634; CA919176.1; -  
 CC PIR; T40526; T40526.  
 CC GeneDB; Spombe; SPBC530.10C; -  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mltc\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH CARRIER; 2.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 28 48 1 (POTENTIAL).  
 FT TRANSMEM 93 111 2 (POTENTIAL).  
 FT TRANSMEM 131 151 3 (POTENTIAL).  
 FT TRANSMEM 197 217 4 (POTENTIAL).  
 FT TRANSMEM 222 242 5 (POTENTIAL).  
 FT TRANSMEM 289 309 6 (POTENTIAL).  
 SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;  
 Query Match 49.8%; Score 770; DB 1; Length 322;  
 Best Local Similarity 53.6%; Pred. No. 2.3e-60;  
 Matches 158; Conservative 51; Mismatches 74; Indels 12; Gaps 6;  
 QY 7 SPANDFLAGVAAAIKSTAVAPIERVKLLQVQ--HASKQTADKQYGIIDCVIRPK 63  
 DB 26 TFPDFPMGVSAAVSKTAAPRIEVRKLLIONQ--DEMIRAGRLSHRYKGIIDCFKRTTAA 83  
 QY 64 EGVLSFWRGNLANVIRYPTQALNFAFKDKYQIIFLGVDKRTQFWRYFAGNLAAGGA 123  
 DB 84 EGVLSFWRGNLANVIRYPTQALNFAFKDKYQIIFLGVDKRTQFWRYFAGNLAAGGA 142  
 QY 124 GATSLCVVYLDPAFRTIADV--VGKAGAREFRGLDCLVKYKSGIKGLYQGFVNSV 181  
 DB 143 GAASLLEVYSLDPAFRTIADV--VGKAGAREFRGLDCLVKYKSGIKGLYQGFVNSV 202

QY 182 QGIIYRAAYFGIYDTAKG-MLPDPKNTHTIVSMIAQTVAAGLTSYPTVRRMM 240  
 DB 203 VGIIVYRGILYFGMYDTLKPVLVGPVLEGNFLASFLGNAVLTGSGVASPLDITRRMM 262  
 QY 241 QSGRGTDIMYGTLDCKWKIARDGGAFFGAGSNVLRGNGAFVLYDEIK 295  
 DB 263 TSGEA---VKTSSECCGRQILAKGARSFFGAGANNLRGVAAGVLSYDQV 314

RESULT 15

ADT\_CHARE STANDARD; PRT; 308 AA.  
 AC P27080;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE ADP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT).  
 GN ABT.  
 OC Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FUD4-R2;  
 RX MEDLINE=93204887; PubMed=8455552;  
 RA Sharpe J.A., Day A.;  
 RT "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii";  
 RL Mol. Gen. Genet. 237:134-144(1993).  
 CC -1 FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
 CC -1 SUBUNIT: Homodimer.  
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1 SIMILARITY: Belongs to the mitochondrial carrier family.

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 CC -----  
 DR EMBL; X65194; CAA46311.1; -  
 DR PIR; S30259; S30259.  
 DR InterPro; IPR002067; Mtc carrier.  
 DR InterPro; IPR001993; MitoCh carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 2.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 74 92 2 (POTENTIAL).  
 FT TRANSMEM 116 133 3 (POTENTIAL).  
 FT TRANSMEM 178 197 4 (POTENTIAL).  
 FT TRANSMEM 217 234 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 49.5%; Score 765; DB 1; Length 308;

Best Local Similarity 52.6%; Pred. No. 66-60; 78; Indels 16; Gaps 6;  
 Matches 159; Conservative 49; Mismatches 78; Indels 16; Gaps 6;

QY 7 SPKDFLAGVAAAIKSTVAPIERVKLLQVQ-HASKQITADKQYKGIIDCVRIPEKQ 65  
 DB 7 NFMVDFLAGGSAASKTAIERVKLLIQNDEMIRKGRSLAPYKIGECFVTVREE 66  
 QY 66 EYLSFWRGNLANVIRYPTQALNFAFKDKIKQIFLGVDKRTQFWRYFAGNLASGAGAA 125

DB 67 GFGSLMRNTANVIRYPTQALNFAFKDKIKQMF--GNNKQETWKMFAGNASGAGAA 124  
 QY 126 TSLCFVYPLDPAKTRTLAD---VGKAGAEERFGRGDLVYIKYSDGIRGLYOGFNVSQ 182  
 DB 125 VLSFVYSLDVARTRLANDASAKKGGDRQFNGLVVDYRKTIASDGIAGIRGFNISCV 184  
 QY 183 GIITRYRAAYFGIYDTAKG-MLPDPKNTHTIVSMIAQTVAAGLTSYPTVRRMMQ 241  
 DB 185 GIVVYRGILYFGMYDLSLKPVLVGPVLEGNFLASFLGNAVLTGSGVASPLDITRRMM 244  
 QY 242 SGRKGTIDIMYGTLDCKWKIARDGGAFFGAGSNVLRGNGAFVLYDEI-----K 295  
 DB 245 S---GSAVKINSFRFCQEIYKNGSKSLFKGAGANNLRGVAAGVLSYDQVYLILGK 301  
 QY 296 KY 297  
 DB 302 KY 303

Search completed: December 18, 2003, 12:41:24  
 Job time : 9.34267 secs



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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:34:56 ; Search time 35.3729 Seconds  
(without alignments)  
1337.197 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543  
Sequence: 1 MTEQAIAPKACFLAGGIAA.....LRKGGAFLVLYDELKKVI 298

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneeqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1543	100.0	298 21	AAAY71033 Human adenine nucl
2	1543	100.0	298 22	AAAM39641 Human polypeptide
3	1543	100.0	298 22	AAU01200 Human adenine nucl
4	1543	100.0	298 23	AAU01380 Human adenine nucl
5	1543	100.0	323 22	AAWA1427 Human-polypeptide
6	1463	94.8	298 23	AAO18516 Human insulin rece
7	1454	94.2	298 21	AAAY71032 Human adenine nucl
8	1454	94.2	298 22	AAU01199 Human adenine nucl
9	1454	94.2	298 23	AAU010379 Human adenine nucl

10	1418	91.9	429	24	ABR41715	Human DITRP organe
11	1412	91.5	298	19	AAK61169	Anti protein. Mus
12	1406	91.1	293	22	ABU53219	Human metacoliem-a
13	1385.5	89.8	297	21	AAAY71031	Human adenine nucl
14	1385.5	89.8	297	22	AAU01198	Human adenine nucl
15	1385.5	89.8	297	23	AAU01378	Human adenine nucl
16	1367.5	88.6	325	22	ABG35423	Novel human diagno
17	1288	83.5	263	22	ABG37056	Novel human diagno
18	1254.5	81.3	299	22	ABBE6082	Drosophila melanog
19	1254.5	81.3	299	22	ABBE7300	Drosophila melanog
20	1137.5	73.7	307	22	ABBS8380	Human metacoliem-a
21	1119	72.5	315	23	ABU53218	Human TRICH-19 pro
22	1119	72.5	315	23	AAE21175	Human TRICH-19 pro
23	1044	67.7	228	23	ABPA3205	Human ovarian anti
24	981	63.6	222	23	ABP74106	Human TRICH SEQ ID
25	879.5	57.0	298	22	ABG18922	Novel human diagno
26	788.5	51.1	301	23	ABP73357	Candida albicans e
27	763	49.4	484	22	ABG35422	Novel human diagno
28	763	49.4	484	22	ABG37055	Novel human diagno
29	749.5	48.6	386	22	AAAG0106	ADP/ATP carrier pr
30	743	48.2	379	24	ABP81267	Arabidopsis thalia
31	742.5	48.1	346	21	AAAG36577	Arabidopsis thalia
32	742.5	48.1	346	21	AAAG37261	Arabidopsis thalia
33	742.5	48.1	346	21	AAAG37264	Arabidopsis thalia
34	742.5	48.1	346	21	AAAG38460	Arabidopsis thalia
35	742.5	48.1	363	21	AAAG36576	Arabidopsis thalia
36	742.5	48.1	363	21	AAAG37260	Arabidopsis thalia
37	742.5	48.1	363	21	AAAG37263	Arabidopsis thalia
38	742.5	48.1	363	21	AAAG38459	Arabidopsis thalia
39	742.5	48.1	381	21	AAAG36575	Arabidopsis thalia
40	742.5	48.1	381	21	AAAG37259	Arabidopsis thalia
41	742.5	48.1	381	21	AAAG37262	Arabidopsis thalia
42	742.5	48.1	381	21	AAAG38458	Arabidopsis thalia
43	742.5	48.1	992	21	AAAG38672	Arabidopsis thalia
44	742.5	48.1	1009	21	AAAG38671	Arabidopsis thalia
45	742.5	48.1	1027	21	AAAG38670	Arabidopsis thalia

## ALIGNMENTS

RESULT 1	AAAY71033	standard; Protein; 298 AA.
ID	AAAY71033	
XX	AAAY71033;	
AC	AAAY71033;	
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DT	29-AUG-2000	(first entry)
XX		
DB	Human adenine nucleotide translocator ANT3.	
XX		
KW	Human, adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;	
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MP; cancer;	
KW	mitochondrial permeability transition; neuroprotective; neurotropic;	
KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;	
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW	mitochondrial diabetes and deafness; hypereproliferative disorder;	
KW	myoclonic epilepsy red ragged fibre syndrome.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200026370-A2.	
XX		
PD	11-MAY-2000.	
XX		
XX	03-NOV-1999;	99WO-US25883.
XX		
XX	03-NOV-1998;	98US-0185904.
PR	08-SEP-1999;	99US-0393441.
XX		

PA (MITO-) MITOKOR.  
 XX  
 PI Anderson CM, Davis RE, Clevenger W, Wiley SR, Miller SM, Szabo TR,  
 PI Ghosh SS;  
 XX WPI, 2000-365619/31.  
 DR N-PSDB; AAD00521.  
 XX  
 PT Recombinant construct encoding adenine nucleoside translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease -  
 XX  
 XX Claim 46; Page 173-174; 175pp; English.  
 XX  
 XX The patent discloses a method to produce adenine nucleoside translocator  
 XX (ANT) proteins or ANT fusion proteins using recombinant expression  
 XX constructs. ANT is a nuclear encoded protein and a major component of  
 XX inner mitochondrial membrane. It mediates transport of adenosine  
 XX di/tri-phosphates across the mitochondrial inner membrane and also serves  
 XX as an important molecular component of the mitochondrial permeability  
 XX transition pore, a modulator of apoptosis. ANT is used to identify agents  
 XX or ligands that bind to, or interact with it. The ANT ligands are used to  
 XX detect or isolate ANT in a biological sample, and therapeutically for  
 XX regulating mitochondrial pore activity, for treating diseases associated  
 XX with altered mitochondrial function, including Alzheimer's, Parkinson's  
 XX and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 XX Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 XX encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 XX disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 XX epilepsy red ragged fibre syndrome. The present sequence is an  
 XX adenine nucleoside translocator ANT3 from human brain.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 100.0%; Score 1543; DB 21; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTEQAIISFAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHASKOIADKQYGI VDCIYR 60  
 DB 1 MTEQAIISFAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHASKOIADKQYGI VDCIYR 60  
 QY 61 IPKEQGVISFWRGNIANTVIRYPTQALNPAFDKTKQIFLGVDVHTQTFWRYFAENL ASG 120  
 DB 61 IPKEQGVISFWRGNIANTVIRYPTQALNPAFDKTKQIFLGVDVHTQTFWRYFAENL ASG 120  
 QY 121 GAAAGTSLCFYVPLDPFARTRLAADVGKSTREPRGLDGLCVKTKSGIRGLYQGF SVS 180  
 DB 121 GAAAGTSLCFYVPLDPFARTRLAADVGKSTREPRGLDGLCVKTKSGIRGLYQGF SVS 180  
 QY 181 VGGIITVRAAFVGVYDTAKGMLPDPKNTHTIVVSMIAQTVTAVAGVSYFPD TVARRMM 240  
 DB 181 VGGIITVRAAFVGVYDTAKGMLPDPKNTHTIVVSMIAQTVTAVAGVSYFPD TVARRMM 240  
 QY 241 OSGRKADIMYTGTDCKWKIRIRDBSGKAFPGKANSNVRGNGAFVLYLDELK VYI 298  
 DB 241 OSGRKADIMYTGTDCKWKIRIRDBSGKAFPGKANSNVRGNGAFVLYLDELK VYI 298  
 RESULT 2  
 AAM39641  
 ID AAM39641 standard; Protein; 298 AA.  
 XX  
 AC AAM39641;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 2786.  
 XX  
 DE Human; nocrotic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Tang YR, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao Q, Zhou P, Goodrich R, Dermanac RT;  
 XX WPI, 2001-442253/47.  
 DR N-PSDB; AA158797.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 XX Example 4; SEQ ID NO 2786; 10078pp; English.  
 XX  
 XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 XX the encoded polypeptides (AAM36642-AA42213) with nocrotic,  
 XX immunosuppressant and cytostatic activity. The polynucleotides are useful  
 XX in gene therapy. A composition containing a polypeptide or polynucleotide  
 XX of the invention may be used to treat diseases of the peripheral nervous  
 XX system, such as peripheral nervous injuries, peripheral neuropathy and  
 XX localized neuropathies and central nervous system diseases, such as  
 XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 XX utilization of the activities such as: immune system suppression,  
 XX Activin/inhibin activity, chemotactic/chemokine activity, haemostatic  
 XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 XX assays for receptor activity, arthritis and inflammation, leukaemia and  
 XX C.N.S disorders  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 CC  
 SQ Sequence 298 AA;  
 Query Match 100.0%; Score 1543; DB 22; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTEQAIISFAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHASKOIADKQYGI VDCIYR 60  
 DB 1 MTEQAIISFAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHASKOIADKQYGI VDCIYR 60  
 QY 61 IPKEQGVISFWRGNIANTVIRYPTQALNPAFDKTKQIFLGVDVHTQTFWRYFAENL ASG 120  
 DB 61 IPKEQGVISFWRGNIANTVIRYPTQALNPAFDKTKQIFLGVDVHTQTFWRYFAENL ASG 120  
 QY 121 GAAAGTSLCFYVPLDPFARTRLAADVGKSTREPRGLDGLCVKTKSGIRGLYQGF SVS 180  
 DB 121 GAAAGTSLCFYVPLDPFARTRLAADVGKSTREPRGLDGLCVKTKSGIRGLYQGF SVS 180  
 QY 181 VGGIITVRAAFVGVYDTAKGMLPDPKNTHTIVVSMIAQTVTAVAGVSYFPD TVARRMM 240  
 DB 181 VGGIITVRAAFVGVYDTAKGMLPDPKNTHTIVVSMIAQTVTAVAGVSYFPD TVARRMM 240  
 QY 241 OSGRKADIMYTGTDCKWKIRIRDBSGKAFPGKANSNVRGNGAFVLYLDELK VYI 298  
 DB 241 OSGRKADIMYTGTDCKWKIRIRDBSGKAFPGKANSNVRGNGAFVLYLDELK VYI 298

Qy 241 QSGRKADIMVTGVDGCRKIFRDEGKAFPGKAMSVLRMGAFVLYVDELKVI 238  
 Db 241 QSGRKADIMVTGVDGCRKIFRDEGKAFPGKAMSVLRMGAFVLYVDELKVI 238

RESULT 3  
 ID AAU01200 standard; Protein; 298 AA.  
 AC AAU01200;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.  
 XX  
 KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200132876-A2.  
 XX  
 PD 10-MAY-2001.  
 XX  
 PE 03-NOV-2000; 2000WO-US30535.  
 XX  
 PR 03-NOV-1999; 99US-0434354.  
 XX  
 PA (MITO-) MITOKOR.  
 XX  
 PI Murphy AM, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;  
 PI Veliceljebl G, Davis RE;  
 PI MPI; 2001-291054/30.  
 DR N-PSDB; AAS05903.  
 XX  
 PT New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 XX  
 PS Disclosure; Fig 2; 186pp; English.  
 XX  
 CC The present sequence represents human adenine nucleotide translocator-3  
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability  
 CC transition (MPT) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.  
 CC  
 XX Sequence 298 AA;  
 Qy Query Match 100.0%; Score 1543; DB 22; Length 298;  
 Beet Local Similarity 100.0%; Pred. No. 4.6e-157;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTEQAISFAKDFLAGIAAIASTKTAVAPIERVKLLQVQHASKOIAADKQYKIVDCIVR 60  
 |||  
 |||

Db 1 MTEQAISFAKDFLAGIAAIASTKTAVAPIERVKLLQVQHASKOIAADKQYKIVDCIVR 60  
 Qy 61 IPKQGLTSPFRGLAVIRVFPQALNFAKDKYKQIFLGVDNKHQPFMYEPGNLASG 120  
 Db 61 IPKQGLTSPFRGLAVIRVFPQALNFAKDKYKQIFLGVDNKHQPFMYEPGNLASG 120  
 Qy 121 GAAGNTSLCFVYPADPARRLAAADVGSCTEERFGLGDCIVKTKSDGIRGLYQGFSSVS 180  
 Db 121 GAAGNTSLCFVYPADPARRLAAADVGSCTEERFGLGDCIVKTKSDGIRGLYQGFSSVS 180  
 Qy 181 VQGIITVRAAFVGYVDTAKGMLPDPKXTHIVSWMIAQTVTAAGVVSYPEDTVRRMM 240  
 Db 181 VQGIITVRAAFVGYVDTAKGMLPDPKXTHIVSWMIAQTVTAAGVVSYPEDTVRRMM 240

Qy 241 QSGRKADIMVTGVDGCRKIFRDEGKAFPGKAMSVLRMGAFVLYVDELKVI 238  
 Db 241 QSGRKADIMVTGVDGCRKIFRDEGKAFPGKAMSVLRMGAFVLYVDELKVI 238

RESULT 4  
 ID AAU0380 standard; Protein; 298 AA.  
 AC AAU0380;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human adenine nucleotide translocator 3 (ANT3).  
 XX  
 KW Human; adenine nucleotide translocator; ANT;  
 KW mitochondrial matrix protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200185944-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PE 11-MAY-2001; 2001WO-US15416.  
 XX  
 PR 11-MAY-2000; 2000US-0569327.  
 XX  
 PA (MITO-) MITOKOR.  
 XX  
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;  
 PI MPI; 2002-055598/07.  
 DR N-PSDB; AAS16690.  
 XX  
 PT Novel recombinant expression construct for producing adenine nucleotide  
 PT translocator polypeptides, comprises a regulated promoter linked to  
 PT nucleic acid encoding the polypeptide -  
 XX  
 PS Example 3; Fig 2; 147pp; English.  
 XX  
 CC The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT3.

XX SQ Sequence 298 AA;  
 Query Match 100.0%; Score 1543; DB 23; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 60  
 DB 1 MTEQAIISPAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 60  
 QY 61 IPKEQGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDVGHGTQFWRFPAGNLASG 120  
 DB 61 IPKEQGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDVGHGTQFWRFPAGNLASG 120  
 QY 121 GAAGATSLCFYYPDLPARTRLAADVGSKSTEREFRLGDCLVKTKSGIRGLYQGFVS 180  
 DB 121 GAAGATSLCFYYPDLPARTRLAADVGSKSTEREFRLGDCLVKTKSGIRGLYQGFVS 180  
 QY 181 VQGIITRYRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQTVTAVAGVSYPPDVTARRMM 240  
 DB 181 VQGIITRYRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQTVTAVAGVSYPPDVTARRMM 240  
 QY 241 QSGRGADIMYTGTVDCWRKIFRDEGGAFFKGAWSNVLKRGGAFFVLVLYDELKCVI 298  
 DB 241 QSGRGADIMYTGTVDCWRKIFRDEGGAFFKGAWSNVLKRGGAFFVLVLYDELKCVI 298

RESULT 5  
 AAM41427  
 ID AAM41427 standard; Protein; 323 AA.  
 AC AAM41427;  
 XX 22-OCT-2001 (first entry)  
 DT Human polypeptide SEQ ID NO 6358.  
 DE Human polypeptide SEQ ID NO 6358.  
 XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX Homo sapiens.  
 OS WO200153312-A1.  
 PN 26-JUL-2001.  
 PD 26-DEC-2000; 2000WO-US34263.  
 PF 21-JAN-2000; 2000US-0486725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 PA (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Aundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;  
 XX WPI; 2001-442253/47.  
 DR N-PSDB; AAI60583.  
 XX Novel nucleic acids and polypeptides; useful for treating disorders  
 PT such as central nervous system injuries -

XX PS Example 2; SEQ ID NO 6358; 10078bp; English.  
 XX CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nocotropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX SQ Sequence 323 AA;  
 Query Match 100.0%; Score 1543; DB 22; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-157;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 60  
 DB 26 MTEQAIISPAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 85  
 QY 61 IPKEQGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDVGHGTQFWRFPAGNLASG 120  
 DB 86 IPKEQGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDVGHGTQFWRFPAGNLASG 145  
 QY 121 GAAGATSLCFYYPDLPARTRLAADVGSKSTEREFRLGDCLVKTKSGIRGLYQGFVS 180  
 DB 146 GAAGATSLCFYYPDLPARTRLAADVGSKSTEREFRLGDCLVKTKSGIRGLYQGFVS 205  
 QY 181 VQGIITRYRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQTVTAVAGVSYPPDVTARRMM 240  
 DB 206 VQGIITRYRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQTVTAVAGVSYPPDVTARRMM 265  
 QY 241 QSGRGADIMYTGTVDCWRKIFRDEGGAFFKGAWSNVLKRGGAFFVLVLYDELKCVI 298  
 DB 266 QSGRGADIMYTGTVDCWRKIFRDEGGAFFKGAWSNVLKRGGAFFVLVLYDELKCVI 323

RESULT 6  
 AAO18516  
 ID AAO18516 standard; Protein; 298 AA.  
 AC AAO18516;  
 XX 11-OCT-2002 (first entry)  
 DT Human insulin receptor signaling modifier SEQ ID NO: 54.  
 DE Human insulin receptor signaling modifier; insulin receptor signaling modifier;  
 KW Human; insulin receptor signaling; insulin receptor signaling modifier;  
 KW ISM; diabetes; metabolic syndrome; antidiabetic.  
 XX Homo sapiens.  
 OS WO200255664-A2.  
 PN 18-JUL-2002.  
 PD 11-JAN-2002; 2002WO-US01048.  
 PF 12-JAN-2001; 2001US-261226P.  
 PR 12-JAN-2001; 2001US-261303P.  
 PR 12-JAN-2001; 2001US-261304P.  
 PR 12-JAN-2001; 2001US-261335P.  
 PR 12-JAN-2001; 2001US-261336P.

PR 12-JAN-2001; 2001US-261361P.  
 PR 12-JAN-2001; 2001US-261456P.  
 PR 12-JAN-2001; 2001US-261457P.  
 PR 12-JAN-2001; 2001US-261458P.  
 PR 12-JAN-2001; 2001US-261459P.  
 PR 12-JAN-2001; 2001US-261461P.  
 PR 12-JAN-2001; 2001US-261518P.  
 PR 12-JAN-2001; 2001US-261531P.  
 PR 12-JAN-2001; 2001US-261532P.  
 PR 12-JAN-2001; 2001US-261589P.  
 PR 12-JAN-2001; 2001US-261590P.  
 PR 12-JAN-2001; 2001US-261694P.  
 PR 12-JAN-2001; 2001US-261695P.  
 PR 12-JAN-2001; 2001US-261697P.  
 XX (EXBL-) EXBLIXIS INC.  
 PA Seidel-Dugan C, Ferguson KC, Kidd T;  
 PI WPI; 2002-599664/64.  
 DR N-PSDB; AAL46635.  
 XX  
 PT Identifying an insulin receptor signaling modulator, useful as drug  
 PT targets for treating diabetes or metabolic disorders, comprises  
 PT contacting an assay system comprising insulin receptor signaling  
 PT modifiers with a test agent -  
 XX  
 PS Disclosure; Page 160-161; 232pp; English.  
 XX  
 CC The present invention relates to a method of identifying a candidate  
 CC insulin receptor (INR) signaling modulating agent, involving contacting  
 CC an assay system comprising an insulin receptor signaling modifier (ISM)  
 CC polypeptide or nucleic acid with a test agent, and detecting a test  
 CC agent-biased activity of the assay system. The method is useful for  
 CC identifying candidate INR signaling modulating agents. ISM genes may be  
 CC used as drug targets for treatment of disorders related to INR signaling  
 CC such as diabetes or metabolic syndrome. ISM nucleic acids and  
 CC polypeptides are useful for identifying and testing agents that modulate  
 CC ISM function and for other applications related to the involvement of ISM  
 CC in INR signaling, and for identifying subjects having a predisposition to  
 CC such diseases associated with INR signaling. The present sequence is an  
 CC ISM protein described in the exemplification of the invention.  
 XX  
 SO Sequence 298 AA;  
 Query Match 94.8%; Score 1463; DB 23; Length 298;  
 Best Local Similarity 92.9%; Pred. No. 1.8e-148;  
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MTEQAISPAKDFLAGGIAAISTKAVAPIERVKLLQVQASKQIADKQYGVDCIVR 60  
 DB 1 MTDAAVSPADKFLAGGVAASISTKAVAPIERVKLLQVQASKQIADKQYGVDCIVR 60  
 QY 1 IPKEGVLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 DB 61 IPKEGVLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 QY 121 GAAGATSLCFYVPLDPAFTRILADVKGSGTEREFGDCLVKTISDGIKGLYOGFSEVS 180  
 DB 121 GAAGATSLCFYVPLDPAFTRILADVKGSGTEREFGDCLVKTISDGIKGLYOGFSEVS 180  
 QY 121 VOGIITVYAAAFRGVYDTAKGMLPDPKNTNTHIVSNMIAQTVAVALTSPDYARRRMM 240  
 DB 181 VOGIITVYAAAFRGVYDTAKGMLPDPKNTNTHIVSNMIAQTVAVALTSPDYARRRMM 240  
 QY 241 QSGRGKADIMTGVDCWRKIFRDEGKAFKFGAWSNVLKRGGAFLVLYDELKK 296  
 DB 241 QSGRGKADIMTGVDCWRKIFRDEGKAFKFGAWSNVLKRGGAFLVLYDELKK 296

XX AAY71032;  
 AC 29-AUG-2000 (first entry)  
 DT Human adenine nucleotide translocator ANT2.  
 XX  
 DE Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;  
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
 KW myoclonic epilepsy red ragged fibre syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200026370-A2.  
 XX  
 XX 11-MAY-2000.  
 XX  
 XX 03-NOV-1999; 99WO-US25863.  
 XX  
 XX 03-NOV-1998; 98US-0185904.  
 XX  
 XX 08-SEP-1999; 99US-0393441.  
 XX  
 XX (MITO-) MITOKOR.  
 XX  
 XX Anderson CM, Davis RE, Cleverger W, Wiley SB, Miller SW, Szabo TR;  
 PI Ghosh S;  
 DR WPI; 2000-365619/31.  
 XX N-PSDB; AAD00520.  
 XX  
 PT Recombinant construct encoding adenine nucleotide translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease -  
 XX  
 PS Claim 45; Page 172-173; 175pp; English.  
 XX  
 CC The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression of  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT2 from human brain.  
 XX  
 SO Sequence 298 AA;  
 Query Match 94.2%; Score 1454; DB 21; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MTEQAISPAKDFLAGGIAAISTKAVAPIERVKLLQVQASKQIADKQYGVDCIVR 60  
 DB 1 MTDAAVSPADKFLAGGVAASISTKAVAPIERVKLLQVQASKQIADKQYGVDCIVR 60  
 QY 61 IPKEGVLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120

Db 61 IPKGEVLSFWKGNLANVIRFPPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPLDPFARTRLAADVGKAGBERFRGLDCLVKITKSDGIRGLYOGFSVS 180  
 QY 181 VGGIITRYAAVFGYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGVVSFPDTPVRRMM 240  
 Db 181 VGGIITRYAAVFGYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGVVSFPDTPVRRMM 240  
 QY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFPKGAMSNVLRGGAFLVLYDELAK 296  
 Db 241 OSGRKADIMTGTVDCKRKIFRDEGKAFPKGAMSNVLRGGAFLVLYDELAK 296

RESULT 8  
 AAU01199  
 ID AAU01199 standard; Protein; 298 AA.

AC AAU01199;  
 DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-2 (ANT-2) protein.

KM Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;  
 KM mitochondrial permeability transition pore component; cell survival;  
 KM mitochondrial core component; mitochondrial related disorder; cancer;  
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.

PN WO200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000MO-US30535.

PR 03-NOV-1999; 99US-0434354.

PA (MITO-) MITOKOR.

PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;  
 PI Velicelebi G, Davis RE;

DR MPI; 2001-291054/30.  
 DR N-PSDB; AAS05902.

PT New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 PS Disclosure; Fig 2; 186pp; English.

CC The present sequence represents human adenine nucleotide translocator-2  
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability  
 CC transition (MPT) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,

CC hyperproliferative disorders e.g. cancer, and deafness.

XX SQ Sequence 298 AA;

Query Match 94.2%; Score 1454; DB 22; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQISPAKDFLAGGIAAISKTAIVADIERVKLLQVQASKOIADQKQYIVDCTVR 60  
 Db 1 MTDALSPAKDFLAGGVAIAISKTAIVADIERVKLLQVQASKOIADQKQYIIDCVVR 60

QY 61 IPKGEVLSFWKGNLANVIRFPPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120  
 Db 61 IPKGEVLSFWKGNLANVIRFPPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120

QY 121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPLDPFARTRLAADVGKAGBERFRGLDCLVKITKSDGIRGLYOGFSVS 180

QY 181 VGGIITRYAAVFGYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGVVSFPDTPVRRMM 240  
 Db 181 VGGIITRYAAVFGYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGVVSFPDTPVRRMM 240

QY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFPKGAMSNVLRGGAFLVLYDELAK 296  
 Db 241 OSGRKADIMTGTVDCKRKIFRDEGKAFPKGAMSNVLRGGAFLVLYDELAK 296

RESULT 9  
 AAU0379  
 ID AAU0379 standard; Protein; 298 AA.

AC AAU0379;  
 DT 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 2 (ANT2).

KM Human; adenine nucleotide translocator; ANT; ss;  
 KM mitochondrial matrix protein.

OS Homo sapiens.

PN WO200185944-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001MO-US15416.

PR 11-MAY-2000; 2000US-0569327.

PA (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;  
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;

DR MPI; 2002-055598/07.  
 DR N-PSDB; AAS16689.

PT Novel recombinant expression construct for producing adenine nucleotide  
 PT translocator polypeptides, comprises a regulated promoter linked to  
 PT nucleic acid encoding the polypeptide -

PS Claim 44; Fig 2; 147pp; English.

CC The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT2.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 94.2%; Score 1454; DB 23; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MTEQAISPAKDFLAGIAAIAISKTAAPIERVKLLQVQHASKOIADKQKGYDCTIVR 60  
 DB 1 MTDALSPAKDFLAGIAAIAISKTAAPIERVKLLQVQHASKOITADKQKGYDCTIVR 60  
 QY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFDKTKQIFLGVDKHTQFMRYFAGNLASG 120  
 DB 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFDKTKQIFLGVDKHTQFMRYFAGNLASG 120  
 QY 121 GAAAGTSLCFVYPLDPARTRLAADVGKSGTERBERGLDCLVKITKSDGIRGLVQGFVS 180  
 DB 121 GAAAGTSLCFVYPLDPARTRLAADVGKSGTERBERGLDCLVKITKSDGIRGLVQGFVS 180  
 QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPPDYRRMM 240  
 DB 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPPDYRRMM 240  
 QY 241 OSGRKADIMTYGTVDCKRKIRDEGKAFKFGANSNVLKMGAPVLVDELKX 296  
 DB 241 OSGRKADIMTYGTVDCKRKIRDEGKAFKFGANSNVLKMGAPVLVDELKX 296  
 DB 241 OSGRKADIMTYGTVDCKRKIRDEGKAFKFGANSNVLKMGAPVLVDELKX 296  
 RESULT 10  
 ABR41715  
 ID ABR41715 standard; Protein; 429 AA.  
 XX  
 AC ABR41715;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE Human DITHP organelle-associated protein.  
 XX  
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
 KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW organelle-associated protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297031-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 27-MAR-2002; 2002WO-US10056.  
 XX  
 PR 28-MAR-2001; 2001US-279619P.  
 PR 29-MAR-2001; 2001US-280067P.  
 PR 29-MAR-2001; 2001US-280068P.  
 PR 16-MAY-2001; 2001US-291280P.  
 PR 17-MAY-2001; 2001US-291829P.  
 PR 17-MAY-2001; 2001US-291849P.  
 PR 19-JUN-2001; 2001US-299428P.  
 PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J,  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PS, Amesley SR,  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH,  
 PI Peraltas CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B,  
 PI Flores V, Marwaha R, Lo A, Lan RX, Urashka ME,  
 XX  
 DR WPI; 2003-129518/12.  
 DR N-PsDB; ACC46652.  
 XX  
 PT Novel human diagnostic and therapeutic polypeptide useful for  
 PT identifying test compound which specifically binds to a polypeptide  
 PT encoded by human diagnostic and therapeutic polynucleotide, and to  
 PT induce antibodies -  
 XX  
 PS Claim 27; SEQ ID No 1250; 591pp; English.  
 XX  
 CC The invention relates to novel human diagnostic and therapeutic  
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their  
 CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates  
 CC to polynucleotide sequences at least 90% identical to the dithp cDNA  
 CC sequences of the invention; recombinant vectors, host cells and  
 CC transgenic organisms comprising a dithp nucleic acid sequence; the  
 CC recombinant production of DITHP proteins; antibodies specific for DITHP  
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods  
 CC of detecting dithp nucleotide and protein sequences; methods of screening  
 CC for compounds which specifically bind a DITHP protein; and methods of  
 CC assessing the toxicity of test compounds using a dithp hybridisation  
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
 CC diagnosis of a wide variety of conditions including cancer and other cell  
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
 CC disorders; neurological disorders; gastrointestinal disorders; transport  
 CC disorders; and connective tissue disorders. They may also be used to  
 CC screen for modulators of protein activity or gene expression. DITHP  
 CC proteins can additionally be used in analysis of the proteome of a tissue  
 CC or cell type and to induce antibodies. The dithp nucleic acids are  
 CC additionally useful in somatic or germline gene therapy of the disorders  
 CC mentioned above, as a source of antisense sequences, as a source of  
 CC probes and primers, in genotyping and identification of individuals, in  
 CC the generation of transgenic animal models of human disease or knock in  
 CC in humanised animals, in toxicological testing, and in transcript imaging.  
 CC The present sequence represents a DITHP protein which is an organelle-  
 CC associated protein.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 429 AA;  
 Query Match 91.9%; Score 1418; DB 24; Length 429;  
 Best Local Similarity 95.2%; Pred. No. 2e-143;  
 Matches 277; Conservative 3; Mismatches 5; Indels 6; Gaps 2;  
 QY 1 MTEQAISPAKDFLAGIAAIAISKTAAPIERVKLLQVQHASKOIADKQKGYDCTIVR 60  
 DB 26 MTEQAISPAKDFLAGIAAIAISKTAAPIERVKLLQVQHASKOIADKQKGYDCTIVR 85  
 QY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFDKTKQIFLGVDKHTQFMRYFAGNLASG 120  
 DB 86 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFDKTKQIFLGVDKHTQFMRYFAGNLASG 145  
 QY 121 GAAAGTSLCFVYPLDPARTRLAADVGKSGTERBERGLDCLVKITKSDGIRGLVQGFVS 180  
 DB 146 GAAAGTSLCFVYPLDPARTRLAADVGKSGTERBERGLDCLVKITKSDGIRGLVQGFVS 205  
 QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPPDYRRMM 240  
 DB 206 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPPDYRRMM 265



QY 241 QSGRGADIMTGTVDGKRIFRDEGKAFKGA-W-----SNVLRGKGA 285  
 DB 266 QSGRGADIMTGTVDGKRIFRDEGKAFKGAFFGSHWKATLADALEGSPSA 316

RESULT 11  
 AAW61169 standard; Protein; 298 AA.

XX AAW61169;  
 AC  
 XX  
 DT 28-SEP-1998 (first entry)  
 DE Anti protein.  
 XX  
 XX Anti; Adenine nucleotide translocator; cloning; screening;  
 KM DNA Tag diodeoxy terminator cycle sequencing; oxidative phosphorylation;  
 KM probe; OXPHOS; mitochondria; ADP, ATP; homzygous mutant; myopathy;  
 KM hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;  
 KM lactic acidosis; degenerative muscle disease.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9819714-A1.  
 XX  
 PD 14-MAY-1998.  
 XX  
 PF 31-OCT-1997; 97WO-US19882.  
 XX  
 PR 01-NOV-1996; 96US-0030017.  
 XX  
 PA (UYEM-) UNIV EMORY.  
 XX  
 PI Graham BC, Macgregor GR, Wallace DC;  
 XX  
 DR WPI, 1998-286608/25.  
 DR N-PsDB; AAV36479.  
 XX  
 PT Mice lacking heart-muscle adenine nucleotide translocator protein -  
 PT useful as model for mitochondrial myopathy and hypertrophic  
 PT cardiomyopathy in animals and to test therapeutic compositions or  
 PT gene therapies  
 XX  
 XX Disclosure; Page 39-40; 61pp; English.  
 PS  
 XX  
 CC The present sequence is the mouse Anti protein, the cDNA producing this  
 CC polypeptide is cloned by screening a mouse heart cDNA library with the  
 CC human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA  
 CC Tag diodeoxy terminator cycle sequencing. The Anti protein is encoded by  
 CC the Anti locus, a nuclear gene on chromosome 8. This protein is required  
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP  
 CC which can then be converted into ATP. An Anti homozygous mutant would  
 CC thus be defective in OXPHOS which results in disease in oxidative  
 CC metabolism dependent tissues. This mouse Anti homozygous mutant can be  
 CC used as a model system for fascioscapular humeral muscular dystrophy,  
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model  
 CC systems can be used to test possible therapeutic compounds which  
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane  
 CC independent of ANT1.  
 CC  
 XX  
 SQ Sequence 298 AA;

Query Match 91.5%; Score 1412; DB 19; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 5.4e-143;  
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGGIAAISTKVAIPERVKLLQVQHASKOIAADKQYGVDCIVR 60  
 DB 1 MGDQALSTFKDFLAGGIAAASKTAIVAPIERVKLLQVQHASKOISAEKQYGIIDCVVR 60  
 QY 1 PKKGVSFMRGNLANVIRYFPFQALNFAFDKXKQIFLGVDGHTQFWRFAAGNLASG 120  
 DB 1 PKKGVSFMRGNLANVIRYFPFQALNFAFDKXKQIFLGVDGHTQFWRFAAGNLASG 120

QY 121 GAAGATSLCFYYPPLDPAFTRILADVSGSTERBERGLDCLVKTGSDGIRGLYQGESVS 180  
 DB 121 GAAGATSLCFYYPPLDPAFTRILADVSGKSSORBERFGLDCLVKTGSDGIRGLYQGESVS 180

QY 181 VOGIITVAAAFYGYDPAKGMPLDPKNTHTIVSNMIAQTVAVAVGVSPPTVARRRMM 240  
 DB 181 VOGIITVAAAFYGYDPAKGMPLDPKNTHTIVSNMIAQSVTAVAGLVSPPTVARRRMM 240

QY 241 QSGRGADIMTGTVDGKRIFRDEGKAFKGAFFGSHWKATLADALEGSPSA 316  
 DB 241 QSGRGADIMTGTVDGKRIFRDEGKAFKGAFFGSHWKATLADALEGSPSA 316

RESULT 12  
 ABUS3219 standard; Protein; 293 AA.

XX ABUS3219;  
 AC  
 XX  
 DT 14-APR-2003 (first entry)  
 DE Human metabolism-associated DKFzpte3\_35n12 homologue #1.  
 KM Human, gene therapy; vaccine; disease treatment; detection.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200112659-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-IB01496.  
 XX  
 PR 18-AUG-1999; 99US-0149499.  
 PR 28-SEP-1999; 99US-0156503.  
 XX  
 PA (GERH-) GERMAN HUMAN GENOME PROJECT.  
 XX  
 PI Wiemann S;  
 XX  
 DR WPI, 2001-327840/34.  
 XX  
 PT Nucleic acids having the sequences of clones isolated from libraries of  
 PT different human tissues, useful in recombinant DNA methodologies -  
 XX  
 XX Example III; Page 850; 1095pp; English.  
 PS  
 XX  
 CC This invention describes novel polynucleotides and polypeptides isolated  
 CC from human cDNA libraries which can be used for gene therapy or in  
 CC vaccines. The polynucleotides of the invention and antibodies encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. The products of the  
 CC invention may also be used to identify modulators of expression and  
 CC activity and to down regulate expression and activity. The antibodies of  
 CC the invention may also be used as diagnostic agents for detecting the  
 CC presence of polypeptides in samples. This sequence represents a homologue  
 CC of a polypeptide described in the disclosure of the invention.  
 CC  
 XX  
 SQ Sequence 293 AA;

Query Match 91.1%; Score 1406; DB 22; Length 293;  
 Best Local Similarity 90.1%; Pred. No. 2.3e-142;  
 Matches 263; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

QY 5 AISAFAKDFLAGGIAAISTKVAIPERVKLLQVQHASKOIAADKQYGVDCIVR 64  
 DB 1 AISAFAKDFLAGGIAAISTKVAIPERVKLLQVQHASKOISAEKQYGIIDCVVR 60  
 QY 65 QGVLSFMRGNLANVIRYFPFQALNFAFDKXKQIFLGVDGHTQFWRFAAGNLASG 124  
 DB 65 QGVLSFMRGNLANVIRYFPFQALNFAFDKXKQIFLGVDGHTQFWRFAAGNLASG 120



QY 125 ATSLCFVYPLDPFARTRLADVKGSGTEREFRGLADCLVKTSGDIRGLYQGFVSVYGI 184  
 DB 121 ATSLCFVYPLDPFARTRLADVKGSGTEREFRGLADCLVKTSGDIRGLYQGFVSVYGI 180  
 QY 185 IIRAAVFGVYDPAKGLPDPKNTTHIVSWMIAQTVAVAGVSYPTVRRMMQSGR 244  
 DB 181 IIRAAVFGVYDPAKGLPDPKNTTHIVSWMIAQTVAVAGVSYPTVRRMMQSGR 240  
 QY 245 KGADIMTYGTVDCKRKIFRDEGSKAFPKGAMSNVLRMGGAFLVLYDELK 296  
 DB 241 KGADIMTYGTVDCKRKIFRDEGSKAFPKGAMSNVLRMGGAFLVLYDELK 292

## RESULT 13

AAV71031  
 ID AAV71031 standard; Protein; 297 AA.  
 AC AAV71031;  
 XX 29-AUG-2000 (first entry)  
 DT  
 XX Human adenine nucleotide translocator ANTI.  
 DE  
 XX Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;  
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
 KW mitochondrial permeability transition; neuroprotective; neurotrophic;  
 KW antiParkinsonian; cyrostatic; antidiabetic; anticonvulsant; neurolytic;  
 KW antiparkinson; cerebroprotective; therapeutic; screening; psoriasis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
 KW myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

MO200026370-A2.

11-MAY-2000.

03-NOV-1999; 99WO-US25883.

03-NOV-1998; 98US-0185904.  
 PR 08-SEP-1999; 99US-0393441.

(MITO-) MITOKOR.

Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,  
 PI Ghosh SS;  
 DR WPI; 2000-365619/31.  
 DR N-PSDB; AAD00519.

Recombinant construct encoding adenine nucleotide translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease -

Claim 44; Page 172; 175pp; English.

The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/citri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative

CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANTI from human brain.

SQ Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 21; Length 297;  
 Best Local Similarity 87.2%; Pred. No. 3.8e-140;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALSPAKDFLAGIAAISKTAIVAPIERVKLLLOVQHASKOIADKQYKIVDCIVR 60  
 DB 1 MGDHAWSEFLKDFLAGAIAAIVSKTAIVAPIERVKLLLOVQHASKOISAEKQYKIIDCVR 60  
 QY 61 IPKEQVLSFWRGLNAVIRFPFOALNPAKDKYKQIFLGQVNRKHPFMYPPAGNLSG 120  
 DB 61 IPKEQVLSFWRGLNAVIRFPFOALNPAKDKYKQIFLGQVNRKHPFMYPPAGNLSG 120  
 QY 121 GAAGATSLCFVYPLDPFARTRLADVKGSGTEREFRGLADCLVKTSGDIRGLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDPFARTRLADVGR-AQREPHGLADCLVKTSGDIRGLYQGFVS 179  
 QY 181 VQGIIRAAVFGVYDPAKGLPDPKNTTHIVSWMIAQTVAVAGVSYPTVRRMM 240  
 DB 180 VQGIIRAAVFGVYDPAKGLPDPKNTTHIVSWMIAQSVTAVALSTYPTVRRMM 239  
 QY 241 QSGRKADIMTYGTVDCKRKIFRDEGSKAFPKGAMSNVLRMGGAFLVLYDELK 298  
 DB 240 QSGRKADIMTYGTVDCKRKIAKDEGAKAFPKGAMSNVLRMGGAFLVLYDEIK 297

## RESULT 14

AAU01198 standard; Protein; 297 AA.

AAU01198;

07-SEP-2001 (first entry)

Human adenine nucleotide translocator-1 (ANT-1) protein.

Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

Homo sapiens.

MO200132876-A2.

10-MAY-2001.

03-NOV-2000; 2000WO-US30535.

03-NOV-1999; 99US-043354.

(MITO-) MITOKOR.

Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritzer LG;  
 PI Velicelcebi G, Davis RE;WPI; 2001-291054/30.  
 DR N-PSDB; AAS05901.

New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -

Disclosure; Fig 2; 186pp; English.

The present sequence represents human adenine nucleotide translocator-1  
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability

CC translation (MTP) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC translocation and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.

CC Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 22; Length 297;

Best Local Similarity 87.2%; Pred. No. 3.8e-140;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALISPAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKQIAADKQYGIYDCIVR 60  
 DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVVR 60  
 QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKTKQIFLGVDVHKTFWRYFAGNLASG 120  
 DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKTKQIFLGVDVHKTFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPARTRLADVGVKSGTEREPRGLGDCLVKITSQDINGLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDPARTRLADVGVKSGTEREPRGLGDCLVKITSQDINGLYQGFVS 179  
 QY 161 VQGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVNSYPTVRRMM 240  
 DB 161 VQGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSNMIAQSVTAAGVNSYPTVRRMM 239  
 QY 241 QSGRKGADIMYTGTVDCMRKIKADEGAKAFKAGMSNVLKMGCAFVLVYDELKQVI 298  
 DB 240 QSGRKGADIMYTGTVDCMRKIKADEGAKAFKAGMSNVLKMGCAFVLVYDEIKQV 297

RESULT 15

AAU10378 standard; Protein; 297 AA.

AAU10378;

14-FEB-2002 (first entry)

Human adenine nucleotide translocator 1 (ANT1).

Human; adenine nucleotide translocator; ANT;

mitochondrial matrix protein.

Homo sapiens.

WO200185944-A2.

15-NOV-2001.

11-MAY-2001; 2001WO-US15416.

11-MAY-2000; 2000US-0569327.

(MITO-) MITOKOR.

Andersen CM, Davis RE, Clevenger W, Wiley SB, Miller SM, Szabo TR,  
 Ghosh SS, Moos WH, Pei Y, Carroll AK;

DR MPT; 2002-055598/07.  
 DR N-PSDB; AAS16688.

Novel recombinant expression construct for producing adenine nucleotide  
 translocator polypeptides, comprises a regulated promoter linked to  
 nucleic acid encoding the polypeptide

Claim 44, Fig 2, 147bp; English.

The invention relates to a recombinant expression construct (1)  
 comprising a regulated promoter operably linked to a nucleic acid  
 encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 proteins mediate the exchange of ATP synthesised in the mitochondrial  
 matrix for ADP in the cytosol. (1) is useful for producing recombinant  
 ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 culturing the host cell. (1) is also useful for targeting a polypeptide  
 of interest to a mitochondrial membrane, where ANT polypeptide is  
 expressed as a fusion protein with the polypeptide of interest.  
 Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 useful for identifying an agent that binds to an ANT polypeptide. ANT  
 ligand is useful for determining the presence of an ANT polypeptide,  
 preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 ANT from a biological sample, where the ANT ligand is covalently or non-  
 covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 useful for identifying an agent that interacts with an ANT polypeptide.  
 The present sequence represents the amino acid sequence of human ANT1.

CC Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 23; Length 297;

Best Local Similarity 87.2%; Pred. No. 3.8e-140; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALISPAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKQIAADKQYGIYDCIVR 60  
 DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVVR 60  
 QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKTKQIFLGVDVHKTFWRYFAGNLASG 120  
 DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKTKQIFLGVDVHKTFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPARTRLADVGVKSGTEREPRGLGDCLVKITSQDINGLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDPARTRLADVGVKSGTEREPRGLGDCLVKITSQDINGLYQGFVS 179  
 QY 161 VQGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVNSYPTVRRMM 240  
 DB 161 VQGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSNMIAQSVTAAGVNSYPTVRRMM 239  
 QY 241 QSGRKGADIMYTGTVDCMRKIKADEGAKAFKAGMSNVLKMGCAFVLVYDELKQVI 298  
 DB 240 QSGRKGADIMYTGTVDCMRKIKADEGAKAFKAGMSNVLKMGCAFVLVYDEIKQV 297

Search completed: December 18, 2003, 12:40:47  
 Job time : 36.3729 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: December 18, 2003, 12:38:52 ; Search time 12.3471 Seconds

(without alignments)  
1021.178 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543  
Sequence: 1 MTEGALISFADFLAGGIAA.....LRGKGAFVLVYDELKKVI 298

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

1: Issued Patents AA: \*  
2: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/PCITUS\_COMB.pep: \*  
7: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	4	US-09-434-354-49 Sequence 49, App1
2	1454	94.2	298	4	US-09-434-354-48 Sequence 48, App1
3	1412	91.5	298	3	US-08-961-871-10 Sequence 10, App1
4	1385.5	89.8	297	4	US-09-434-354-47 Sequence 47, App1
5	314	20.3	469	4	US-09-996-243-289 Sequence 289, App
6	311	20.2	469	3	US-09-188-930-339 Sequence 339, App
7	311	20.2	469	4	US-09-312-283C-339 Sequence 339, App
8	286	18.5	335	4	US-09-482-273-118 Sequence 118, App
9	283.5	18.4	291	4	US-09-501-558-2 Sequence 2, App1
10	280	18.1	447	4	US-09-160-119-4 Sequence 2, App1
11	280	18.1	674	4	US-09-160-119-2 Sequence 2, App1
12	265	17.2	312	3	US-09-142-565-2 Sequence 2, App1
13	250.5	16.2	299	1	US-08-518-878B-56 Sequence 56, App1
14	250.5	16.2	299	1	US-08-470-868A-56 Sequence 56, App1
15	250.5	16.2	309	1	US-08-518-878B-51 Sequence 51, App1
16	250.5	16.2	309	2	US-08-807-861A-51 Sequence 51, App1
17	250.5	16.2	309	2	US-08-470-868A-51 Sequence 51, App1
18	250.5	16.2	309	2	US-08-210-681-51 Sequence 51, App1
19	250.5	16.2	309	3	US-08-946-719A-51 Sequence 51, App1
20	250.5	16.2	309	4	US-09-547-983-51 Sequence 51, App1
21	250.5	16.2	311	2	US-08-775-009-33 Sequence 33, App1
22	245	15.9	432	2	US-08-937-466-4 Sequence 4, App1
23	245	15.9	432	2	US-08-172-528-4 Sequence 4, App1
24	245	15.9	432	3	US-09-318-199-4 Sequence 4, App1
25	244	15.8	432	3	US-09-503-579-4 Sequence 4, App1
26	244	15.8	308	2	US-08-937-466-2 Sequence 2, App1
27	244	15.8	308	2	US-09-172-528-2 Sequence 2, App1

28	244	15.8	308	3	US-09-318-199-2 Sequence 2, App1
29	244	15.8	308	3	US-09-503-579-2 Sequence 2, App1
30	243.5	15.8	311	2	US-08-775-009-32 Sequence 32, App1
31	232.5	15.1	320	2	US-08-933-750C-12 Sequence 12, App1
32	232.5	15.1	320	3	US-09-234-613-12 Sequence 12, App1
33	227.5	14.7	303	1	US-08-294-522B-36 Sequence 36, App1
34	226.5	14.7	303	2	US-08-518-878B-37 Sequence 37, App1
35	226.5	14.7	303	2	US-08-807-861A-37 Sequence 37, App1
36	226.5	14.7	303	2	US-08-470-868A-37 Sequence 37, App1
37	226.5	14.7	303	3	US-09-210-681-37 Sequence 37, App1
38	226.5	14.7	303	3	US-08-946-719A-37 Sequence 37, App1
39	226.5	14.7	303	4	US-09-547-983-37 Sequence 37, App1
40	222	14.4	293	4	US-09-501-558-4 Sequence 4, App1
41	211	13.7	306	5	PCT-US94-09799-1 Sequence 1, App1
42	205.5	13.3	307	2	US-08-807-861A-56 Sequence 56, App1
43	205.5	13.3	307	3	US-09-210-681-56 Sequence 56, App1
44	205.5	13.3	307	3	US-08-946-719A-56 Sequence 56, App1
45	205.5	13.3	307	4	US-09-547-983-56 Sequence 56, App1

## ALIGNMENTS

RESULT 1  
US-09-434-354-49

Sequence 49, Application US/09434354

Patent No. 6562563

GENERAL INFORMATION:

APPLICANT: Murphy, Anne N.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Andreyev, Alexander Y.

APPLICANT: Frigetti, Luciano G.

APPLICANT: Velicelebi, Gonul

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING

TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR

TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS

FILE REFERENCE: 660088.433

CURRENT APPLICATION NUMBER: US/09/434,354

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 49

LENGTH: 298

TYPE: PRT

ORGANISM: Homo sapien

US-09-434-354-49

Query Match 100.0%; Score 1543; DB 4; Length 298;

Best Local Similarity 100.0%; Pred. No. 4.5e-166; Mismatches 0; Indels 0; Gaps 0;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTEGALISFADFLAGGIAAISKTAIVPIRVKLLLOVQASQIADKQYKGIIVDCIVR	60
DB	1	MTEGALISFADFLAGGIAAISKTAIVPIRVKLLLOVQASQIADKQYKGIIVDCIVR	60
QY	61	IPKQGVLSFWRGMLANVIRPPTQALNFAFKQYKQIFLGGVDKHTQFRRYFAGNLASG	120
DB	61	IPKQGVLSFWRGMLANVIRPPTQALNFAFKQYKQIFLGGVDKHTQFRRYFAGNLASG	120
QY	121	GAGATSLCTVYPLDPARTLADVQSGTERRERIGDGLVTKSDGIRGLYQGSYS	180
DB	121	GAGATSLCTVYPLDPARTLADVQSGTERRERIGDGLVTKSDGIRGLYQGSYS	180
QY	181	VQGIITIRAAVFGVYDPAKGMPLDPKNTHTLVSMIQTVAAGVSYFPDTRRRMM	240
DB	181	VQGIITIRAAVFGVYDPAKGMPLDPKNTHTLVSMIQTVAAGVSYFPDTRRRMM	240
QY	241	QSGRKGADIMYTGIVDCMRKIFRDEGKAFPKGAMSVNLKMGGAFLVLYDELKKVI	298
DB	241	QSGRKGADIMYTGIVDCMRKIFRDEGKAFPKGAMSVNLKMGGAFLVLYDELKKVI	298

RESULT 2  
US-09-434-354-48  
Sequence 48, Application US/09434354  
Patent No. 6562563  
GENERAL INFORMATION:  
APPLICANT: Murphy, Anne N.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Bileen  
APPLICANT: Andreyev, Alexander Y.  
APPLICANT: Frigeri, Luciano G.  
APPLICANT: Velicelcbl, Gonul  
APPLICANT: Davis, Robert E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
FILE REFERENCE: 660088.433  
CURRENT APPLICATION NUMBER: US/09/434,354  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 48  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-434-354-48

Query Match 94.2%; Score 1454; DB 4; Length 298;  
Best Local Similarity 92.6%; Pred. No. 5.2e-156;  
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQASPAKDFLAGGIAAIAISKTAVAPIERVKLLLOVQHASKOIADKQYKGIYDCIYR 60  
DB 1 MTDALSPAKDFLAGGIAAIAISKTAVAPIERVKLLLOVQHASKOIADKQYKGIYDCIYR 60  
QY 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHGTQFWRYPFAGNLASG 120  
DB 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHGTQFWRYPFAGNLASG 120  
QY 121 GAAGATSLCFYYPIDFPAFTRLAADVKGSGTEREFGDCLVYKTSQDGRGLYOGFSVS 180  
DB 121 GAAGATSLCFYYPIDFPAFTRLAADVKGSGTEREFGDCLVYKTSQDGRGLYOGFSVS 180  
QY 181 VGGIITRAAYFGYVDIAKGLPDPKNTHTIVSMIAQTVTAAGVSVSPEDTVRRMM 240  
DB 181 VGGIITRAAYFGYVDIAKGLPDPKNTHTIVSMIAQTVTAAGVSVSPEDTVRRMM 240  
QY 241 QSGRKGADIMYTGTVDCWKRKIFRDEGGAFFKGAMSNVLRGMGAFVLYDEIKK 296  
DB 241 QSGRKGADIMYTGTVDCWKRKIFRDEGGAFFKGAMSNVLRGMGAFVLYDEIKK 296

## RESULT 3

US-08-961-871-10  
Sequence 10, Application US/08961871  
Patent No. 6013858  
GENERAL INFORMATION:  
APPLICANT: Wallace, Douglas C.  
APPLICANT: Graham, Brett H.  
APPLICANT: MacGregor, Grant R.  
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine  
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,871  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/030,017  
FILING DATE: 01-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 78-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-871-10

Query Match 91.5%; Score 1412; DB 3; Length 298;  
Best Local Similarity 88.6%; Pred. No. 2.9e-151;  
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQASPAKDFLAGGIAAIAISKTAVAPIERVKLLLOVQHASKOIADKQYKGIYDCIYR 60  
DB 1 MTDALSPAKDFLAGGIAAIAISKTAVAPIERVKLLLOVQHASKOIADKQYKGIYDCIYR 60  
QY 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHGTQFWRYPFAGNLASG 120  
DB 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHGTQFWRYPFAGNLASG 120  
QY 121 GAAGATSLCFYYPIDFPAFTRLAADVKGSGTEREFGDCLVYKTSQDGRGLYOGFSVS 180  
DB 121 GAAGATSLCFYYPIDFPAFTRLAADVKGSGTEREFGDCLVYKTSQDGRGLYOGFSVS 180  
QY 181 VGGIITRAAYFGYVDIAKGLPDPKNTHTIVSMIAQTVTAAGVSVSPEDTVRRMM 240  
DB 181 VGGIITRAAYFGYVDIAKGLPDPKNTHTIVSMIAQTVTAAGVSVSPEDTVRRMM 240  
QY 241 QSGRKGADIMYTGTVDCWKRKIFRDEGGAFFKGAMSNVLRGMGAFVLYDEIKK 298  
DB 241 QSGRKGADIMYTGTVDCWKRKIFRDEGGAFFKGAMSNVLRGMGAFVLYDEIKK 298

## RESULT 4

US-09-434-354-47  
Sequence 47, Application US/09434354  
Patent No. 6562563  
GENERAL INFORMATION:  
APPLICANT: Murphy, Anne N.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Bileen  
APPLICANT: Andreyev, Alexander Y.  
APPLICANT: Frigeri, Luciano G.  
APPLICANT: Velicelcbl, Gonul  
APPLICANT: Davis, Robert E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
FILE REFERENCE: 660088.433  
CURRENT APPLICATION NUMBER: US/09/434,354  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Homo sapien

1	PRIOR APPLICATION NUMBER: 60/07891910
2	PRIOR FILING DATE: 1998-03-20
3	PRIOR APPLICATION NUMBER: 60/08332222
4	PRIOR FILING DATE: 1998-04-28
5	PRIOR APPLICATION NUMBER: 60/08460000
6	PRIOR FILING DATE: 1998-05-07
7	PRIOR APPLICATION NUMBER: 60/08710606
8	PRIOR FILING DATE: 1998-05-28
9	PRIOR APPLICATION NUMBER: 60/08760707
10	PRIOR FILING DATE: 1998-06-02
11	PRIOR APPLICATION NUMBER: 60/08760000
12	PRIOR FILING DATE: 1998-06-02
13	PRIOR APPLICATION NUMBER: 60/08775555
14	PRIOR FILING DATE: 1998-06-02
15	PRIOR APPLICATION NUMBER: 60/08782727
16	PRIOR FILING DATE: 1998-06-03
17	PRIOR APPLICATION NUMBER: 60/08802121
18	PRIOR FILING DATE: 1998-06-04
19	PRIOR APPLICATION NUMBER: 60/08802222
20	PRIOR FILING DATE: 1998-06-04
21	PRIOR APPLICATION NUMBER: 60/08802323
22	PRIOR FILING DATE: 1998-06-04
23	PRIOR APPLICATION NUMBER: 60/08803030
24	PRIOR FILING DATE: 1998-06-04
25	PRIOR APPLICATION NUMBER: 60/08803333
26	PRIOR FILING DATE: 1998-06-04
27	PRIOR APPLICATION NUMBER: 60/08832222
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/08816767
30	PRIOR FILING DATE: 1998-06-05
31	PRIOR APPLICATION NUMBER: 60/08820202
32	PRIOR FILING DATE: 1998-06-05
33	PRIOR APPLICATION NUMBER: 60/08821212
34	PRIOR FILING DATE: 1998-06-05
35	PRIOR APPLICATION NUMBER: 60/08821313
36	PRIOR FILING DATE: 1998-06-05
37	PRIOR APPLICATION NUMBER: 60/08855555
38	PRIOR FILING DATE: 1998-06-09
39	PRIOR APPLICATION NUMBER: 60/08873434
40	PRIOR FILING DATE: 1998-06-10
41	PRIOR APPLICATION NUMBER: 60/08873838
42	PRIOR FILING DATE: 1998-06-10
43	PRIOR APPLICATION NUMBER: 60/08882222
44	PRIOR FILING DATE: 1998-06-10
45	PRIOR APPLICATION NUMBER: 60/08874242
46	PRIOR FILING DATE: 1998-06-10
47	PRIOR APPLICATION NUMBER: 60/08881010
48	PRIOR FILING DATE: 1998-06-10
49	PRIOR APPLICATION NUMBER: 60/08882222
50	PRIOR FILING DATE: 1998-06-10
51	PRIOR APPLICATION NUMBER: 60/08882323
52	PRIOR FILING DATE: 1998-06-10
53	PRIOR APPLICATION NUMBER: 60/08885555
54	PRIOR FILING DATE: 1998-06-11
55	PRIOR APPLICATION NUMBER: 60/08886161
56	PRIOR FILING DATE: 1998-06-11
57	PRIOR APPLICATION NUMBER: 60/08887676
58	PRIOR FILING DATE: 1998-06-11
59	PRIOR APPLICATION NUMBER: 60/08910505
60	PRIOR FILING DATE: 1998-06-12
61	PRIOR APPLICATION NUMBER: 60/08944444
62	PRIOR FILING DATE: 1998-06-16
63	PRIOR APPLICATION NUMBER: 60/08951212
64	PRIOR FILING DATE: 1998-06-16
65	PRIOR APPLICATION NUMBER: 60/08951414
66	PRIOR FILING DATE: 1998-06-16
67	PRIOR APPLICATION NUMBER: 60/08953333
68	PRIOR FILING DATE: 1998-06-17
69	PRIOR APPLICATION NUMBER: 60/08953838
70	PRIOR FILING DATE: 1998-06-17
71	PRIOR APPLICATION NUMBER: 60/08959696



Db 297 SIYMEVLTAKTMA--LRKTG---QYSGMLDCARRILAKESGAAPYKGIYIPNNLGIIPYAG 351  
 QY 190 AYFGVDTAKGMLPDPKNTI-----VYSMMIAQTVTVAG--VVSYPDTYRRR 237  
 Db 352 IDLAVETL-----KNTWLQRYAVNSADGCVFVLACGTTISCTGGLASYPPLAVRTR 404  
 QY 238 MMQSGRGKADIMYTGTVDCWRKIFRDEGKAFKFGKAMSNVLRGKGAFV-LVLYDELX 295  
 Db 405 MQAQSIEGAPEVTMSSL--FKQILRTGAGFGLYRGLAPNPKVIYPAVISISVYVENLK 461

# RESULT 7

US-09-312-283C-339

Sequence 339, Application US/09312283C  
 Patent No. 6573095  
 GENERAL INFORMATION:

APPLICANT: Watson, James D.  
 APPLICANT: Strachan, Lorna  
 APPLICANT: Sleeman, Matthew  
 APPLICANT: Onrust, Rene  
 APPLICANT: Murison, James G.  
 APPLICANT: Kumble, Krishanand D.  
 TITLE OF INVENTION: Compositions Isolated from Skin Cells  
 TITLE OF INVENTION: and Methods for Their Use  
 FILE REFERENCE: 11000.1011C2  
 CURRENT APPLICATION NUMBER: US/09/312,283C  
 CURRENT FILING DATE: 1999-05-14  
 NUMBER OF SEQ ID NOS: 425  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 339  
 LENGTH: 469  
 TYPE: PRT  
 ORGANISM: Mouse  
 US-09-312-283C-339

Query Match 20.2%; Score 311; DB 4; Length 469;  
 Best Local Similarity 29.4%; Pred. No. 1.7e-26;  
 Matches 86; Conservative 62; Mismatches 111; Indels 38; Gaps 11;

QY 10 KDFLAGGIAAIAISTAVAPIERVKLLIQVHASQIADKQYKIVDCIARIPIKQVLS 69  
 Db 188 RHVAGGAGAVSRTCTAPDLRLKVMQV--HASSR-----SNMKCIYGGFTGIMREGAKS 241  
 QY 70 FMRGNLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSAGGAAGATSLC 129  
 Db 242 LMRGNINVLKIAESAIKFAAYEQMKR--LVGSDQET--LRHERLVASGLAGALAQOS 296  
 QY 130 FVYELDPARTLADVKGSGTEREFGLDCLVKTISDGRGHYOGFSVSVQGIITYRA 189  
 Db 297 SIYMEVLTAKTMA--LRKTG---QYSGMLDCARRILAKESGAAPYKGIYIPNNLGIIPYAG 351  
 QY 190 AYFGVDTAKGMLPDPKNTI-----VYSMMIAQTVTVAG--VVSYPDTYRRR 237  
 Db 352 IDLAVETL-----KNTWLQRYAVNSADGCVFVLACGTTISCTGGLASYPPLAVRTR 404  
 QY 238 MMQSGRGKADIMYTGTVDCWRKIFRDEGKAFKFGKAMSNVLRGKGAFV-LVLYDELX 295  
 Db 405 MQAQSIEGAPEVTMSSL--FKQILRTGAGFGLYRGLAPNPKVIYPAVISISVYVENLK 461

# RESULT 8

US-09-482-273-118

Sequence 118, Application US/09482273  
 Patent No. 6534631  
 GENERAL INFORMATION:

APPLICANT: Rosen et al.  
 TITLE OF INVENTION: 71 Human Secreted Proteins  
 FILE REFERENCE: P2030B1  
 CURRENT APPLICATION NUMBER: US/09/482,273  
 CURRENT FILING DATE: 2000-01-13  
 EARLIER APPLICATION NUMBER: PCT/US99/15849  
 EARLIER FILING DATE: 1999-07-14  
 EARLIER APPLICATION NUMBER: 60/092,921

EARLIER FILING DATE: 1998-07-15  
 EARLIER APPLICATION NUMBER: 60/092,922  
 EARLIER FILING DATE: 1998-07-15  
 EARLIER APPLICATION NUMBER: 60/092,956  
 EARLIER FILING DATE: 1998-07-15  
 NUMBER OF SEQ ID NOS: 267  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 118  
 LENGTH: 335  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (335)  
 OTHER INFORMATION: Xaa equals stop translation  
 US-09-482-273-118

Query Match 18.5%; Score 286; DB 4; Length 335;  
 Best Local Similarity 29.0%; Pred. No. 6.9e-24;  
 Matches 87; Conservative 50; Mismatches 133; Indels 30; Gaps 8;

QY 10 KDFLAGGIAAIAISTAVAPIERVKLLIQVHAS-----KQIADKQYKIVDCIARIPIKE 64  
 Db 51 KPEVYGGIASIVAFEGTFPVDLTETRLQVQGSIDARFKEI---KTRGMFHALFRICKE 106  
 QY 65 QGVLSFMRGNLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSAGGAAG 124  
 Db 107 EGVLAISGIALPALRQASGTITIGIYQSLKRLVERLDET-----LLIMICGVAVSG 161  
 QY 125 ATSLCFYPLDPARTLADVKGSGTEREFGLDCLVKTISDGRGHYOGFSVSVQGI 184  
 Db 162 VISSTIANPVDVLRKIRQA-----QGLFQGSMTGS-FIDYQSGTRGMRGVPTIQA 216  
 QY 185 IYRAVFGVYDTAK-----GMLPDPKNTIIVVSMIAQTVTVAGVVSYPDTYRRR 238  
 Db 217 AIVGVGLPVDITKRLILSGMMGDTILTFVSSF-----TCGLAGALASNPVDVVRTRM 272  
 QY 239 MMQSGRGKADIMYTGTVDCWRKIFRDEGKAFKFGKAMSNVLR-GMGAFVLVLYDELX 297  
 Db 273 MQRALVGHVDLTKIGIVDGILKMKHKGFPALYKGFPMNLRLGPMNIIFPITYEQLRL 332

# RESULT 9

US-09-501-558-2

Sequence 2, Application US/09501558  
 Patent No. 6403784  
 GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander Jr.  
 APPLICANT: Mathur, Brian  
 APPLICANT: Zambrowicz, Brian  
 APPLICANT: Sands, Arthur T.  
 TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and  
 FILE REFERENCE: LEX-0012-USA  
 CURRENT APPLICATION NUMBER: US/09/501,558  
 CURRENT FILING DATE: 2000-02-09  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 2  
 LENGTH: 291  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-501-558-2

Query Match 18.4%; Score 283.5; DB 4; Length 291;  
 Best Local Similarity 28.9%; Pred. No. 1.1e-23;  
 Matches 87; Conservative 54; Mismatches 129; Indels 31; Gaps 9;

QY 10 KDFLAGGIAAIAISTAVAPIERVKLLIQVHAS-----KQIADKQYKIVDCIARIPIKE 64  
 Db 7 KPEVYGGIASIVAFEGTFPVDLTETRLQVQGSIDARFKEI---KTRGMFHALFRICKE 106  
 QY 65 QGVLSFMRGNLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSAGGAAG 124

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Db      63 EQLKLYSGIAPAMLRQASVGTIKIGTQSLRLRLTERPEDET-----LPINVICGISG 117
Qy      125 ATSLCFVPLPDLFARTLADVKGSTBERFRGLDCLVTKTSDDIGLYOGFSVSVOGI 184
Db      118 VISSIANPTDVLKIRMOA-----QSNITIQ--GGMINFNMTIYQGBEIRGLMKGVSLTAQRA 172
Qy      185 IIRAYVGVYDTAK-----GMLDPPKXTHIVSMMIAQTAVAGVVSYPFDVRRM 238
Db      173 AIVVGVLPVYDITKKHLILSGIMGDVTVTHFLSSF-----TCGLAGALASNPVDVVRTRM 228
Qy      239 MMQSG-RKGDIMYTGTVDCMRKIFRDEGKAFPFKAGMSNVLR--GMGAFLVLYLDELK 296
Db      229 MNQVLRDGRSGGYTITDCLLQTKMKGFFALYKGFPMNLRGPMNIIFFVTEQLK 288
Qy      297 V 297
Db      289 L 289
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RESULT 10
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-4
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Query Match      18.1%; Score 280; DB 4; Length 447;
Best Local Similarity 27.1%; Pred. No. 5.1e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;

Qy      4 QAI$PAKDFLAGGIAAISTKNAVAPIERYKLLQVQHASKOIADKQYKGIYDCLVRI$PK 63
Db      96 QVABSAVRFGLGSVAGAVATAVPIIDLVKTRMQRSTGSFVGLMVKNSPDCPKVLR 155
Qy      64 BOGVLSFWRGMLANVIRFPTQALNFAFKDKYKQI$FL---GGVDKHTQFWRYFAGNLSAG 120
Db      156 YEGFGLYRGLLPOLLGVAPEKAIKLTYNDFVRDKFMKQSV$P-----LAAELIAG 207
Qy      121 GAAGATSLCFVYPLDLPARTLADVKGSTBERFRGLDCLVTKTSDDIGLYOGFSVS 180
Db      208 GCAGSGVITFNTPLFIIVKIRLQV-AGEITTGPRVSAL-----SVVRDGLGFGIYKGAAC 261
Qy      181 VQGIITIRAAVFGYVDTAKGMLPDPKXTHIVSMMIAQTVTA$V-AGVVSYPFDVRRM 239
Db      262 FLRDI$P$AIYFPCYAHVKS$FANEDQVSPGSLILAGALGMPAASLVTPADVYKTR-- 319
Qy      240 MOSGRKADIMYTGTVDCMRKIFRDEGKAFPFKAGMSNVLRGMA$FVLYLDEL 294
Db      320 LQVAA$AGQTTYS$GVIDCFRKLIREBGRKALMKAGARV$FSS$PQFVTLTLTYEL 374
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RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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```
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-2
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Query Match      18.1%; Score 280; DB 4; Length 674;
Best Local Similarity 27.1%; Pred. No. 9.4e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;

Qy      4 QAI$PAKDFLAGGIAAISTKNAVAPIERYKLLQVQHASKOIADKQYKGIYDCLVRI$PK 63
Db      323 QVABSAVRFGLGSVAGAVATAVPIIDLVKTRMQRSTGSFVGLMVKNSPDCPKVLR 382
Qy      64 BOGVLSFWRGMLANVIRFPTQALNFAFKDKYKQI$FL---GGVDKHTQFWRYFAGNLSAG 120
Db      383 YEGFGLYRGLLPOLLGVAPEKAIKLTYNDFVRDKFMKQSV$P-----LAAELIAG 434
Qy      121 GAAGATSLCFVYPLDLPARTLADVKGSTBERFRGLDCLVTKTSDDIGLYOGFSVS 180
Db      435 GCAGSGVITFNTPLFIIVKIRLQV-AGEITTGPRVSAL-----SVVRDGLGFGIYKGAAC 488
Qy      181 VQGIITIRAAVFGYVDTAKGMLPDPKXTHIVSMMIAQTVTA$V-AGVVSYPFDVRRM 239
Db      489 FLRDI$P$AIYFPCYAHVKS$FANEDQVSPGSLILAGALGMPAASLVTPADVYKTR-- 546
Qy      240 MOSGRKADIMYTGTVDCMRKIFRDEGKAFPFKAGMSNVLRGMA$FVLYLDEL 294
Db      547 LQVAA$AGQTTYS$GVIDCFRKLIREBGRKALMKAGARV$FSS$PQFVTLTLTYEL 601
```

```
RESULT 12
US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-142-565-2
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Query Match      17.2%; Score 265; DB 3; Length 312;
Best Local Similarity 27.1%; Pred. No. 1.5e-21;
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Matches 82; Conservative 52; Mismatches 145; Indels 24; Gaps 8;

Qy 7 SPADFLAGGTAATSKTAVPIERVKLLQVQ--HASKQIADKQYGVDCYIRIRKE 64  
 Db 12 TMAVFLAGTACADLTTPFLDTAKVRLQIGENQAVQTRALVQYGVGVTILTMVRT 71  
 Qy 65 QGVLSFMRGNLANVIRYPTQALNPAFKDKYKQIFL--GGVDKHTQFMFYPAGNLASGGA 123  
 Db 72 EGPCSPYVGLVAGLORQMSFASIRIGLYDSVKQVTPPKADNSLITTLA-----GCTT 126  
 Qy 124 GATSLCFYVPLDPARTLADV--GKSGTEREFGDGLVKTITKSDIRGLYQFSVS 181  
 Db 127 GAMATCAQPTDVVKVRFOASIHLPSSRSDRCXGTMADYRTIAREEGVRLMGKGLPNI 186  
 Qy 182 OGIIITRYARFQVYPTAKGMLPDPKQTHIVSMIAQVTA-----VAGVSYPPDYTR 236  
 Db 187 MRNALVNCALVVTYILKEKLD---YHLTDNPFCHVPSAFGAFCATVVASPDVYKT 243  
 Qy 237 RMMNQGRRKADIMYTGTCWRKIFRDEGKAPFKGAMSNVLR--GMGAFLVLYDELK 295  
 Db 244 RYM-----NSPPGQYFSPLDCHIKVNAQEGPTAFYKGPFTLRGSMNVVMFTYBOLK 298  
 Qy 296 KVI 298  
 Db 299 RAL 301

RESULT 13  
 US-08-518-878B-56  
 ; Sequence 56, Application US/08518878B  
 ; Patent No. 5702902  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tartaglia, Louis A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TITILE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
 ; NUMBER OF SEQUENCES: 57  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSER: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/518,878B  
 ; FILING DATE: 23-AUG-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7853-036  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 56:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 299 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; US-08-518-878B-56

Query Match 16.2%; Score 250.5; DB 1; Length 299;  
 Best Local Similarity 24.9%; Pred. No. 6e-20;  
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

Qy 12 FLAGGIAAISKTAVPIERVKLLQVOHASK---QIADKQYGVDCYIRIRKEQVL 68  
 Db 7 FLAGGTAACIADLTTPFLDTAKVRLQIGESQGVRAVNSQYGVGVTILTMRTBPR 66  
 Qy 69 SFMRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQFMFYPAGNLASGGAATSL 128  
 Db 67 SLVNGLVAGLORQMSFASVRIGLYDSVKQFYTKG--SEHAS-----IGSRLLAGSTTGALAV 121  
 Qy 129 CFVYPLDPARTLADVCKSGTEREFGDGLVKTITKSDIRGLYQFSVSOGIILYR 188  
 Db 122 AVAQPPTDVVKVRFOAQ--AFAGGRRYOSTVAAYTTIAREEGVRLMGKGSNVAANAVLN 180  
 Qy 189 AAYGVYDTAK-----GMLPDPKQTHIVSMIAQVTAAGVAVSYPPDYTRRMMQMS 242  
 Db 181 CAELVTTDLIDALLKANLMTDDLPCHFTSAFGAFCTTIVAS----PVDVVKTRYM--- 233  
 Qy 243 GRKADIMYTGTCWRKIFRDEGKAPFKGAMSNVLR--GMGAFLVLYDELKVI 298  
 Db 234 --NSALQYSSAGHCALTMLQKEGPRAFYKGPFPMSFLRSGSMNVVMFTYBOLKRAL 288

RESULT 14  
 US-08-470-868A-56  
 ; Sequence 56, Application US/08470868A  
 ; Patent No. 5861485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tartaglia, Louis C.  
 ; TITLE OF INVENTION: Compositions and Methods for the  
 ; TITILE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSER: Pennie and Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/470,868A  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66441 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 56:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 299 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; US-08-470-868A-56

Query Match 16.2%; Score 250.5; DB 2; Length 299;  
 Best Local Similarity 24.9%; Pred. No. 6e-20;  
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

Qy 12 FLAGGIAAISKTAVPIERVKLLQVOHASK---QIADKQYGVDCYIRIRKEQVL 68  
 Db 7 FLAGGTAACIADLTTPFLDTAKVRLQIGESQGVRAVNSQYGVGVTILTMRTBPR 66  
 Qy 69 SFMRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQFMFYPAGNLASGGAATSL 128  
 Db 67 SLVNGLVAGLORQMSFASVRIGLYDSVKQFYTKG--SEHAS-----IGSRLLAGSTTGALAV 121

QY 129 CFVYLPDPAFTPLADVGKSGTEREFGCLVITKITSDDIRGLYQGSVSVOGIIYR 188  
DB 122 AVAQPTDVVKYFQAO-ARAGGRRYQSVNNAKYKTIAREGFRGLMKGSPVNAALAVN 180  
QY 169 AAYFVYDTAK-----GWLDPKXNTHIVSWMIAQTVAVAGVVSYPEDTVRRBMMQMS 242  
DB 181 CAELVTVYDLIKALLKANIMTDDLPCHFTSAGAGCTTVIAS----PVDVVKTRYM--- 233  
QY 243 GRKGADIMYGTVDQWKRKIFRDEGGKAFPKGAMSNVLR-GMGAFVLVLYDELKKVI 298  
DB 234 --NSALQYSSAGHCALTMLQKEGPRAFYKGFMPBFLRSGMNVVMFVLYEQDKRAL 288

RESULT 15  
US-08-518-878B-51  
Sequence 51, Application US/08518878B  
Patent No. 5702902

GENERAL INFORMATION:  
APPLICANT: Tartaglie, Louis A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/518,878B  
FILING DATE: 23-AUG-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-036  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
US-08-518-878B-51

Query Match 16.2%; Score 250.5; DB 1; Length 309;

Best Local Similarity 24.9%; Pred.No. 6.3e-20;

Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISTKTAAPIERVLLLOVOHASK---QIADKQYKGIIVDCIYIRPKQGVL 68  
DB 17 FLGACTAACIADLITFPLDTAKVRLIQESQGPVATVSAQYKGVMTILTMVTEGPR 76  
QY 69 SEWRGNLANVIRYPTQALNFAFKDYKQIFLGVDKHTQFWRYFAGNLAGGAAGATSL 128  
DB 77 SLVNGLVAGLQROMSPASVRIGLYDSVKQFYTKG-SEHAS-----IGSRLIAGSTGALAV 131  
QY 129 CFVYLPDPAFTPLADVGKSGTEREFGCLVITKITSDDIRGLYQGSVSVOGIIYR 188  
DB 132 AVAQPTDVVKYFQAO-ARAGGRRYQSVNNAKYKTIAREGFRGLMKGSPVNAALAVN 190  
QY 189 AAYFVYDTAK-----GWLDPKXNTHIVSWMIAQTVAVAGVVSYPEDTVRRBMMQMS 242  
DB 191 CAELVTVYDLIKALLKANIMTDDLPCHFTSAGAGCTTVIAS----PVDVVKTRYM--- 243

QY 243 GRKGADIMYGTVDQWKRKIFRDEGGKAFPKGAMSNVLR-GMGAFVLVLYDELKKVI 298  
DB 244 --NSALQYSSAGHCALTMLQKEGPRAFYKGFMPBFLRSGMNVVMFVLYEQDKRAL 298

Search completed: December 18, 2003, 12:44:56  
Job time: 13.3471 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:43:17 ; Search time 24.3606 Seconds

(without alignments)  
2284.595 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543  
Sequence: 1 MTEQALSFADPFLAGGIAA.....LRGNGAFVLVYDELKKVI 298

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 166758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubppa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	1543	100.0	298	US-09-811-094-33	Sequence 33, Appl
2	1543	100.0	298	US-09-810-644-33	Sequence 33, Appl
3	1543	100.0	298	US-09-185-904-33	Sequence 33, Appl
4	1454	94.2	298	US-09-811-094-32	Sequence 32, Appl
5	1454	94.2	298	US-09-810-644-32	Sequence 32, Appl
6	1454	94.2	298	US-09-185-904-32	Sequence 32, Appl
7	1385.5	89.8	297	US-09-811-094-31	Sequence 31, Appl
8	1385.5	89.8	297	US-09-810-644-31	Sequence 31, Appl
9	1385.5	89.8	297	US-09-185-904-31	Sequence 31, Appl
10	811	52.6	179	US-10-029-386-32501	Sequence 32501, A
11	788.5	51.1	301	US-10-032-585-7194	Sequence 7194, Ap
12	760.5	49.3	318	US-09-801-568-252	Sequence 252, App
13	749.5	48.6	386	US-09-734-569-170	Sequence 170, App
14	737	47.8	308	US-10-128-714-3338	Sequence 3338, Ap
15	737	47.8	308	US-10-128-714-8338	Sequence 8338, Ap

16	734.5	47.6	381	12	US-10-141-478A-2	Sequence 2, Appl1
17	686	44.5	677	12	US-10-259-165-192	Sequence 192, App
18	518	33.6	132	9	US-09-925-301-1459	Sequence 1459, App
19	423	27.4	87	9	US-09-864-761-36440	Sequence 36440, A
20	368	23.8	475	10	US-09-777-921A-4	Sequence 4, Appl1
21	368	23.8	477	10	US-09-777-921A-2	Sequence 2, Appl1
22	333.5	21.6	410	10	US-09-777-921A-5	Sequence 5, Appl1
23	336	21.1	384	12	US-10-094-749-1789	Sequence 1789, Ap
24	314	20.3	469	9	US-09-989-722-289	Sequence 289, App
25	314	20.3	469	9	US-09-989-723-289	Sequence 289, App
26	314	20.3	469	9	US-09-989-729-289	Sequence 289, App
27	314	20.3	469	9	US-09-989-727-289	Sequence 289, App
28	314	20.3	469	10	US-09-989-732-289	Sequence 289, App
29	314	20.3	469	10	US-09-989-732-289	Sequence 289, App
30	314	20.3	469	10	US-09-991-073-289	Sequence 289, App
31	314	20.3	469	10	US-09-990-442-289	Sequence 289, App
32	314	20.3	469	10	US-09-991-163-289	Sequence 289, App
33	314	20.3	469	10	US-09-993-604-289	Sequence 289, App
34	314	20.3	469	10	US-09-990-456-289	Sequence 289, App
35	314	20.3	469	10	US-09-989-721-289	Sequence 289, App
36	314	20.3	469	10	US-09-992-598-289	Sequence 289, App
37	314	20.3	469	10	US-09-989-293A-289	Sequence 289, App
38	314	20.3	469	10	US-09-989-735-289	Sequence 289, App
39	314	20.3	469	10	US-09-990-444-289	Sequence 289, App
40	314	20.3	469	10	US-09-991-181-289	Sequence 289, App
41	314	20.3	469	10	US-09-989-730-289	Sequence 289, App
42	314	20.3	469	10	US-09-990-436-289	Sequence 289, App
43	314	20.3	469	10	US-09-993-687-289	Sequence 289, App
44	314	20.3	469	11	US-09-989-734-289	Sequence 289, App
45	314	20.3	469	11	US-09-997-653-289	Sequence 289, App

## ALIGNMENTS

RESULT 1  
US-09-811-094-33  
Sequence 33, Application US/09811094  
Patent No. US20010044144A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Miller, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pel, Yashong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),  
FILE REFERENCE: 660088.420D4  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastsEQ for Windows Version 3.0  
SEQ ID NO 33  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-811-094-33  
Query Match 100.0%; Score 1543; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1e-156;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTEQALSFADPFLAGGIAAISTKTAAPRIRVLLQVGHASQIADKQYKGIIVCTIVR 60  
DB 1 MTEQALSFADPFLAGGIAAISTKTAAPRIRVLLQVGHASQIADKQYKGIIVCTIVR 60  
QY 1 IPEQGVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFRFYAGNLASG 120  
DB 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFRFYAGNLASG 120

Qy 121 GAAGATSLCFYPLDPARTLAADVKGSGTEREFGDCLVKTSGDKGLVGGESVS 180  
 Db 121 GAAGATSLCFYPLDPARTLAADVKGSGTEREFGDCLVKTSGDKGLVGGESVS 180  
 Qy 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240  
 Db 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240  
 Qy 241 QSGRKGADIMYTGIVDCWRKIFRDEGKAFFKGAMSVNLKMGAFVLVLYDELKVI 298  
 Db 241 QSGRKGADIMYTGIVDCWRKIFRDEGKAFFKGAMSVNLKMGAFVLVLYDELKVI 298

RESULT 2  
 US-09-810-644-33  
 ; Sequence 33, Application US/09810644  
 ; Patent No. US20020012992A1  
 ; GENERAL INFORMATION:

; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Miller, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Moos, Walter H.  
 ; APPLICANT: Pel, Yazhong  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
 ; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 ; FILE REFERENCE: 660088.420D3  
 ; CURRENT APPLICATION NUMBER: US/09/810.644  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 33  
 ; LENGTH: 298  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-810-644-33

Query Match 100.0%; Score 1543; DB 9; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1e-156;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQAISFADFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYKGIIVDCIVR 60  
 Db 1 MTEQAISFADFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYKGIIVDCIVR 60  
 Qy 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKTKQIFLGVDKHTQFMRYFAGNLASG 120  
 Db 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKTKQIFLGVDKHTQFMRYFAGNLASG 120  
 Qy 121 GAAGATSLCFYPLDPARTLAADVKGSGTEREFGDCLVKTSGDKGLVGGESVS 180  
 Db 121 GAAGATSLCFYPLDPARTLAADVKGSGTEREFGDCLVKTSGDKGLVGGESVS 180  
 Qy 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240  
 Db 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240  
 Qy 241 QSGRKGADIMYTGIVDCWRKIFRDEGKAFFKGAMSVNLKMGAFVLVLYDELKVI 298  
 Db 241 QSGRKGADIMYTGIVDCWRKIFRDEGKAFFKGAMSVNLKMGAFVLVLYDELKVI 298

RESULT 3  
 US-09-185-904A-33  
 ; Sequence 33, Application US/09185904A  
 ; Patent No. US2002017185A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.

; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Miller, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
 ; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
 ; FILE REFERENCE: 660088.420  
 ; CURRENT APPLICATION NUMBER: US/09/185.904A  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 33  
 ; LENGTH: 298  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-185-904A-33

Query Match 100.0%; Score 1543; DB 10; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1e-156;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MTEQAISFADFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYKGIIVDCIVR 60  
 Db 1 MTEQAISFADFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYKGIIVDCIVR 60  
 Qy 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKTKQIFLGVDKHTQFMRYFAGNLASG 120  
 Db 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKTKQIFLGVDKHTQFMRYFAGNLASG 120  
 Qy 121 GAAGATSLCFYPLDPARTLAADVKGSGTEREFGDCLVKTSGDKGLVGGESVS 180  
 Db 121 GAAGATSLCFYPLDPARTLAADVKGSGTEREFGDCLVKTSGDKGLVGGESVS 180  
 Qy 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240  
 Db 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240  
 Qy 241 QSGRKGADIMYTGIVDCWRKIFRDEGKAFFKGAMSVNLKMGAFVLVLYDELKVI 298  
 Db 241 QSGRKGADIMYTGIVDCWRKIFRDEGKAFFKGAMSVNLKMGAFVLVLYDELKVI 298

RESULT 4  
 US-09-811-094-32  
 ; Sequence 32, Application US/09811094  
 ; Patent No. US2001004414A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Miller, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Moos, Walter H.  
 ; APPLICANT: Pel, Yazhong  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
 ; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 ; FILE REFERENCE: 660088.420D4  
 ; CURRENT APPLICATION NUMBER: US/09/811.094  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 32  
 ; LENGTH: 298  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-811-094-32

Query Match 94.2%; Score 1454; DB 9; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 3.5e-147;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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QY 1 MTEOASIFAKOPLAGGAAIAAISTAVAPIERVKLLQVHASKOIAADKQYGYDCTVR 60
  1 MTDALISPAKOPLAGGAAIAAISTAVAPIERVKLLQVHASKOITADKQYGIIDCVVR 60
DB 1 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFMWYFAGNLASG 120
  61 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFMWYFAGNLASG 120
DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKYKSDGIRGLYOGSPVS 180
  121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKYKSDGIRGLYOGSPVS 180
DB 121 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
  181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
QY 181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
  181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
DB 241 QSGRKGADIMYTGVDCKWKIFRDEGKAFFKGAWSNVLKMGAFVLYVDELK 296
  241 QSGRKGADIMYTGVDCKWKIFRDEGKAFFKGAWSNVLKMGAFVLYVDELK 296
```

RESULT 5  
US-09-810-644-32

; Sequence 32, Application US/09810644  
; Patent No. US20020012992A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Christen M.

; APPLICANT: Davis, Robert E.

; APPLICANT: Clevenger, William

; APPLICANT: Wiley, Sandra Eileen

; APPLICANT: Willet, Scott W.

; APPLICANT: Szabo, Tomas R.

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Moos, Walter H.

; APPLICANT: Pel, Yashong

; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),

; FILE REFERENCE: 660088.420D3

; CURRENT APPLICATION NUMBER: US/09/810,644

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 32

; LENGTH: 298

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-810-644-32

Query Match 94.2%; Score 1454; DB 9; Length 298;  
Best Local Similarity 92.6%; Pred. No. 3.5e-147;  
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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QY 1 MTEOASIFAKOPLAGGAAIAAISTAVAPIERVKLLQVHASKOIAADKQYGYDCTVR 60
  1 MTDALISPAKOPLAGGAAIAAISTAVAPIERVKLLQVHASKOITADKQYGIIDCVVR 60
DB 1 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFMWYFAGNLASG 120
  61 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFMWYFAGNLASG 120
DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKYKSDGIRGLYOGSPVS 180
  121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKYKSDGIRGLYOGSPVS 180
DB 121 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
  181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
QY 181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
  181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
DB 241 QSGRKGADIMYTGVDCKWKIFRDEGKAFFKGAWSNVLKMGAFVLYVDELK 296
  241 QSGRKGADIMYTGVDCKWKIFRDEGKAFFKGAWSNVLKMGAFVLYVDELK 296
```

RESULT 6  
US-09-185-904A-32

; Sequence 32, Application US/09185904A  
; Patent No. US20020177185A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Christen M.

; APPLICANT: Davis, Robert E.

; APPLICANT: Clevenger, William

; APPLICANT: Wiley, Sandra Eileen

; APPLICANT: Willet, Scott W.

; APPLICANT: Szabo, Tomas R.

; APPLICANT: Ghosh, Soumitra S.

; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

; TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS

; FILE REFERENCE: 660088.420

; CURRENT APPLICATION NUMBER: US/09/185,904A

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 32

; LENGTH: 298

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-185-904A-32

Query Match 94.2%; Score 1454; DB 10; Length 298;  
Best Local Similarity 92.6%; Pred. No. 3.5e-147;  
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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QY 1 MTEOASIFAKOPLAGGAAIAAISTAVAPIERVKLLQVHASKOIAADKQYGYDCTVR 60
  1 MTDALISPAKOPLAGGAAIAAISTAVAPIERVKLLQVHASKOITADKQYGIIDCVVR 60
DB 1 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFMWYFAGNLASG 120
  61 IPKEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFMWYFAGNLASG 120
DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKYKSDGIRGLYOGSPVS 180
  121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKYKSDGIRGLYOGSPVS 180
DB 121 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
  181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
QY 181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
  181 VOGIIYRAAYFGYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDVRRRMM 240
DB 241 QSGRKGADIMYTGVDCKWKIFRDEGKAFFKGAWSNVLKMGAFVLYVDELK 296
  241 QSGRKGADIMYTGVDCKWKIFRDEGKAFFKGAWSNVLKMGAFVLYVDELK 296
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RESULT 7  
US-09-811-094-31

; Sequence 31, Application US/09811094  
; Patent No. US2001004414A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Christen M.

; APPLICANT: Davis, Robert E.

; APPLICANT: Clevenger, William

; APPLICANT: Wiley, Sandra Eileen

; APPLICANT: Willet, Scott W.

; APPLICANT: Szabo, Tomas R.

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Moos, Walter H.

; APPLICANT: Pel, Yashong

; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),

; FILE REFERENCE: 660088.420D4

; CURRENT APPLICATION NUMBER: US/09/811,094

; NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-811-094-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;  
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKQYGIYDCIVR 60  
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVRR 60  
 QY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVDRHKKQFWRYPAGNLASG 120  
 DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVDRHKKQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFYVPDLPARTRLAADVGKSGTEREFGDLCLVTKSGDGLRGLYOGFSVS 180  
 DB 121 GAAGATSLCFYVPDLPARTRLAADVGR-AGREHFGDLDCIIFKSDGLRGLYOGFSVS 179  
 QY 181 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIVSWMIAGTVTAAGVSPPTVRRMM 240  
 DB 180 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIVSWMIAGTVTAAGVSPPTVRRMM 239  
 QY 241 QSGRGADIMYTGIVDCWRKIFRDEGKAFPKGAMSNVLRMGAFVLVLYDELKVI 298  
 DB 240 QSGRGADIMYTGIVDCWRKIAKDEGAKAFPKGAMSNVLRMGAFVLVLYDEIKKYV 297

# RESULT 8

US-09-810-644-31  
 Sequence 31, Application US/09810644  
 Patent No. US20020012992A1

GENERAL INFORMATION:  
 APPLICANT: Anderson, Christen M.  
 APPLICANT: Davis, Robert E.  
 APPLICANT: Clevenger, William  
 APPLICANT: Wiley, Sandra Eileen  
 APPLICANT: Miller, Scott W.  
 APPLICANT: Szabo, Tomas R.  
 APPLICANT: Ghosh, Soumitra S.  
 APPLICANT: Moos, Walter H.  
 APPLICANT: Pel, Yezhong  
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT'),  
 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 FILE REFERENCE: 660088.420D3  
 CURRENT APPLICATION NUMBER: US/09/810,644  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-810-644-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;  
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKQYGIYDCIVR 60  
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVRR 60  
 QY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVDRHKKQFWRYPAGNLASG 120  
 DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVDRHKKQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFYVPDLPARTRLAADVGKSGTEREFGDLCLVTKSGDGLRGLYOGFSVS 180  
 DB 121 GAAGATSLCFYVPDLPARTRLAADVGR-AGREHFGDLDCIIFKSDGLRGLYOGFSVS 179

DB 121 GAAGATSLCFYVPDLPARTRLAADVGR-AGREHFGDLDCIIFKSDGLRGLYOGFSVS 179  
 QY 181 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIVSWMIAGTVTAAGVSPPTVRRMM 240  
 DB 180 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIVSWMIAGTVTAAGVSPPTVRRMM 239  
 QY 241 QSGRGADIMYTGIVDCWRKIFRDEGKAFPKGAMSNVLRMGAFVLVLYDELKVI 298  
 DB 240 QSGRGADIMYTGIVDCWRKIAKDEGAKAFPKGAMSNVLRMGAFVLVLYDEIKKYV 297

## RESULT 9

US-09-185-904A-31  
 Sequence 31, Application US/09185904A  
 Patent No. US2002017185A1

GENERAL INFORMATION:  
 APPLICANT: Anderson, Christen M.  
 APPLICANT: Davis, Robert E.  
 APPLICANT: Clevenger, William  
 APPLICANT: Wiley, Sandra Eileen  
 APPLICANT: Miller, Scott W.  
 APPLICANT: Szabo, Tomas R.  
 APPLICANT: Ghosh, Soumitra S.  
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
 TITLE OF INVENTION: TRANSLOCATOR (ANT'), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
 TITLE OF INVENTION: THEREFOR  
 FILE REFERENCE: 660088.420  
 CURRENT APPLICATION NUMBER: US/09/185,904A  
 CURRENT FILING DATE: 1998-11-03  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-185-904A-31

Query Match 89.8%; Score 1385.5; DB 10; Length 297;  
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKQYGIYDCIVR 60  
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVRR 60  
 QY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVDRHKKQFWRYPAGNLASG 120  
 DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVDRHKKQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFYVPDLPARTRLAADVGKSGTEREFGDLCLVTKSGDGLRGLYOGFSVS 180  
 DB 121 GAAGATSLCFYVPDLPARTRLAADVGR-AGREHFGDLDCIIFKSDGLRGLYOGFSVS 179  
 QY 181 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIVSWMIAGTVTAAGVSPPTVRRMM 240  
 DB 180 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIVSWMIAGTVTAAGVSPPTVRRMM 239  
 QY 241 QSGRGADIMYTGIVDCWRKIFRDEGKAFPKGAMSNVLRMGAFVLVLYDELKVI 298  
 DB 240 QSGRGADIMYTGIVDCWRKIAKDEGAKAFPKGAMSNVLRMGAFVLVLYDEIKKYV 297

## RESULT 10

US-10-029-386-32501  
 Sequence 32501, Application US/10029386  
 Publication No. US20030194704A1

GENERAL INFORMATION:  
 APPLICANT: Penn, Sharon G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
 TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
 FILE REFERENCE: ASOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 32501  
LENGTH: 179  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC004000.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96  
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU2 2.00e-83  
US-10-029-386-32501

Query Match 52.6%; Score 811; DB 12; Length 179;  
Best Local Similarity 93.3%; Pred. No. 1.2e-78;  
Matches 152; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 38 VQASKQIADKQYKIVDCIVRIPKQGVLSFMRGNLANYRYPTQALNFAFKDKYKQ 97  
DB 1 VQASKQIADKQYKIVDCIVRIPKQGVLSFMRGNLANYRYPTQALNFAFKDKYKQ 60

QY 98 IFLGVDVHTQPMRYFAENLASGGAAGTSLCFYVPLDPARTRLAADVKGSGTEREPGL 157  
DB 61 IFLGVDVHTQPMRYFAENLASGGAAGTSLCFYVPLDPARTRLAADVKGSGTEREPGL 120

QY 158 GDCIVKTKSDIGIRGLYQGSFVSVOGIIITYRAAYGVYDTAKG 200  
DB 121 GDCIVKTKSDIGIRGLYQGSFVSVOGIIITYRAAYGVYDTAKG 163

RESULT 11  
US-10-032-585-7194  
Sequence 7194, Application US/10032585  
Publication No. US20030180953A1  
GENERAL INFORMATION:  
APPLICANT: Terry, Roemer D.  
APPLICANT: Bo, Jlang  
APPLICANT: Charles, Boone  
APPLICANT: Howard, Bussey  
TITLE OR INVENTION: Gene Disruption Methodologies for Drug Target Discovery  
FILE REFERENCE: 10182-005-999  
CURRENT APPLICATION NUMBER: US/10/032,585  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 8000  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7194  
LENGTH: 301  
TYPE: PRT  
ORGANISM: Candida albicans  
US-10-032-585-7194

Query Match 51.1%; Score 788.5; DB 12; Length 301;  
Best Local Similarity 54.7%; Pred. No. 6.3e-76;  
Matches 162; Conservative 42; Mismatches 83; Indels 9; Gaps 5;

QY 7 SFADPLAGGIAAISTKAVAPIERVKLLQVQ-HASKQIADKQYKIVDCIVRIPKQ 65  
DB 5 NFADPLAGGIAAISTKAVAPIERVKLLQVQ-HASKQIADKQYKIVDCIVRIPKQ 64

QY 66 GVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQPMRYFAENLASGGAAGA 125  
DB 65 GVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQPMRYFAENLASGGAAGA 122

QY 126 TSLCFYVPLDPARTRLAADV--GKSGTEREPGLDCLVKTGSDIGIRGLYQGSFVSVOG 183  
DB 123 TSLCFYVPLDPARTRLAADV--GKSGTEREPGLDCLVKTGSDIGIRGLYQGSFVSVOG 182

QY 184 IIVRAAYGVYDTAKG-MLPDPKNTHTIVSWMIAQVTAAGVAVSVYPTVRRRMMQ 242

DB 183 IIVYRGILYFGLYDGLKLVVLVGPLEGSLFSLFLLGAVTTGASTASVPLDVRRRMMQ 242  
QY 243 GRKADIMTGTVDGCMKIFRDBGGKAFPFKGANSVIRGAGAFVLYVDELKVTI 298  
DB 243 GQA---VKYDGAIDCFRKYVAABGVGSLFKGCCANILIRGAVAGVLSLYDQLQVTL 295

RESULT 12  
US-09-801-368-252  
Sequence 252, Application US/09801368  
Patent No. US20020128250A1  
GENERAL INFORMATION:  
APPLICANT: Bueby, Robert  
APPLICANT: Cali, Brian  
APPLICANT: Hecht, Peter  
APPLICANT: Holtzman, Doug  
APPLICANT: Madden, Kevin  
APPLICANT: Maxon, Mary  
APPLICANT: Milne, Todd  
APPLICANT: No. US20020128250A1man, Thea  
APPLICANT: Royer, John  
APPLICANT: Salama, Sofie  
APPLICANT: Sherman, Amir  
APPLICANT: Silva, Jeff  
APPLICANT: Summers, Eric  
TITLE OR INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
FILE REFERENCE: 109272.147  
CURRENT APPLICATION NUMBER: US/09/801,368  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 09/487,558  
PRIOR FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: US 60/160,587  
PRIOR FILING DATE: 1999-10-20  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 252  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
US-09-801-368-252

Query Match 49.3%; Score 760.5; DB 10; Length 318;  
Best Local Similarity 53.7%; Pred. No. 6.8e-73;  
Matches 159; Conservative 42; Mismatches 86; Indels 9; Gaps 5;

QY 7 SFADPLAGGIAAISTKAVAPIERVKLLQVQ-HASKQIADKQYKIVDCIVRIPKQ 65  
DB 22 NFADPLAGGIAAISTKAVAPIERVKLLQVQ-HASKQIADKQYKIVDCIVRIPKQ 81

QY 66 GVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQPMRYFAENLASGGAAGA 125  
DB 82 GVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQPMRYFAENLASGGAAGA 139

QY 126 TSLCFYVPLDPARTRLAADV--GKSGTEREPGLDCLVKTGSDIGIRGLYQGSFVSVOG 183  
DB 140 TSLCFYVPLDPARTRLAADV--GKSGTEREPGLDCLVKTGSDIGIRGLYQGSFVSVOG 199

QY 184 IIVRAAYGVYDTAKG-MLPDPKNTHTIVSWMIAQVTAAGVAVSVYPTVRRRMMQ 242  
DB 200 IIVRAAYGVYDTAKG-MLPDPKNTHTIVSWMIAQVTAAGVAVSVYPTVRRRMMQ 259

QY 243 GRKADIMTGTVDGCMKIFRDBGGKAFPFKGANSVIRGAGAFVLYVDELKVTI 298  
DB 260 GQA---VKYDGAIDCFRKYVAABGVGSLFKGCCANILIRGAVAGVLSLYDQLQVTL 312

RESULT 13  
US-09-734-569-170  
Sequence 170, Application US/09734569  
Patent No. US20020064816A1  
GENERAL INFORMATION:  
APPLICANT: Lerchl, Jens

APPLICANT: Reutz, Andreas  
 APPLICANT: Ehrhardt, Thomas  
 APPLICANT: Reindl, Andreas  
 APPLICANT: Cirus, Petra  
 APPLICANT: Bischoff, Friedrich  
 APPLICANT: Frank, Markus  
 APPLICANT: Freund, Annette  
 APPLICANT: Duwendt, Elke  
 APPLICANT: Schmidt, Ralf-Michael  
 APPLICANT: Reeski, Ralf  
 TITLE OF INVENTION: Moss genes from *Physcomitrella patens* encoding proteins involved  
 FILE REFERENCE: BASF-NAE-1333-99-US  
 CURRENT FILING DATE: 2001-05-24  
 PRIOR APPLICATION NUMBER: US 60/171,101  
 PRIOR FILING DATE: 1999-12-16  
 NUMBER OF SEQ ID NOS: 181  
 SOFTWARE: PatentIn Ver. 2.1/wordperfect 6.1  
 SEQ ID NO: 170  
 LENGTH: 386  
 TYPE: PRT  
 ORGANISM: *Physcomitrella patens*  
 US-09-734-569-170

Query Match 48.6%; Score 749.5; DB 9; Length 386;  
 Best Local Similarity 53.4%; Pred. No. 1.3e-71;  
 Matches 157; Conservative 44; Mismatches 84; Indels 9; Gaps 5;

Cy 7 SPADFLAGIAGIAAISTAVAPIERVKLLQVQ--HASQIADAKQYKGIIVDCIARIK 65  
 Db 84 SPMDFLGGVSAASKTAAPIERVKLLIQVQDEMLKSGRLSHPKYKIGEFSTVQ 143  
 Cy 66 GVLSEFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASGAAGA 125  
 Db 144 GMSLMRGNTANVIRYPTQALNFAFKQYKSLFGYKDK--DGYKWFAGNLASGAAGA 202  
 Cy 126 TSLCFYPLDPAKRTLAADV--GKSGTEREFRGIDCLVKTSGDIRGLYOGFSVSQ 182  
 Db 203 SSLFVVLSDYARITLANDAKSSKKGGERQFNGIVDYKKTLDGIGAGLYRGAISCA 262  
 Cy 183 GIITRYAAYFGVYDPAKG--MLPDPKNTIIVSWMIAGTVTAAGVVSYPPTVRRMMQ 241  
 Db 263 GIITRYGILFYGLDYLKVVVLVGNLEGNFLASFLGKGIITGAGLASPIPIVRRMMQ 322  
 Cy 242 SGRKADIMYTGVDCKRKIFRDEGKAFPKGAMSVNLGNGAFVLVYDELK 295  
 Db 323 SGGA---VKYNGSMDAFKQILAKGAKSLFKGAGANILRAVAGAGVLSGYDQLQ 373

RESULT 14  
 US-10-128-714-3338  
 Sequence 3338, Application US/10128714  
 Publication No. US20030119013A1  
 GENERAL INFORMATION:  
 APPLICANT: Jiang, Bo  
 APPLICANT: Hu, Wengqi  
 APPLICANT: Tishkoff, Daniel  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Eroshkin, Alexey M  
 APPLICANT: Lemieux, Sebastien M  
 TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and  
 FILE REFERENCE: 10182-018-999  
 CURRENT FILING DATE: 2002-04-23  
 PRIOR APPLICATION NUMBER: US/10/128,714  
 PRIOR FILING DATE: 2001-04-23  
 PRIOR APPLICATION NUMBER: US 60/285,697  
 PRIOR FILING DATE: 2001-04-27  
 PRIOR APPLICATION NUMBER: US 60/287,066  
 PRIOR FILING DATE: 2001-04-27  
 PRIOR APPLICATION NUMBER: US 60/295,890  
 PRIOR FILING DATE: 2001-06-05  
 PRIOR APPLICATION NUMBER: US 60/303,899

PRIOR FILING DATE: 2001-07-09  
 PRIOR APPLICATION NUMBER: US 60/316,362  
 PRIOR FILING DATE: 2001-08-31  
 NUMBER OF SEQ ID NOS: 8603  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 3338  
 LENGTH: 308  
 TYPE: PRT  
 ORGANISM: *Aspergillus fumigatus*  
 US-10-128-714-3338

Query Match 47.8%; Score 737; DB 15; Length 308;  
 Best Local Similarity 51.7%; Pred. No. 2.1e-70;  
 Matches 154; Conservative 47; Mismatches 85; Indels 12; Gaps 6;

Cy 7 SPADFLAGIAGIAAISTAVAPIERVKLLQVQHASQIQA--DKQYKGIIVDCIARIK 63  
 Db 7 APTDSFAGVSAVSAKTAAPIERIKL--VQNDQEMIRAGRDRKNGIIDCFRRTAQ 64  
 Cy 64 ECGVLSFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASGAAGA 123  
 Db 65 AEGVMSLMRGNTANVIRYPTQALNFAFKQYKSMFYKKOR--DGYAKMMWGNLASGAAGA 123  
 Cy 124 GATSLCFYPLDPAKRTLAADV--GKSGTEREFRGIDCLVKTSGDIRGLYOGFSVSQ 181  
 Db 124 GATSLFVVLSDYARITLANDAKSAGGERQFNGLIDYRKITLASDGIAGLYRGFQSV 183  
 Cy 182 GGIITRYAAYFGVYDPAKG--MLPDPKNTIIVSWMIAGTVTAAGVVSYPPTVRRMMQ 240  
 Db 184 LGITVYGLYGVWDISKPVVLVGLSGSFLASFLGKGIITGAGIASYPTDITRRMMQ 243  
 Cy 241 QSGRKADIMYTGVDCKRKIFRDEGKAFPKGAMSVNLGNGAFVLVYDELKXY 298  
 Db 244 TSGBA---VKYKSLDAKQILAKGAKSLFKGAGANILRGVAGVLSYDQVLL 298

RESULT 15  
 US-10-128-714-8338  
 Sequence 8338, Application US/10128714  
 Publication No. US20030119013A1  
 GENERAL INFORMATION:  
 APPLICANT: Jiang, Bo  
 APPLICANT: Hu, Wengqi  
 APPLICANT: Tishkoff, Daniel  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Eroshkin, Alexey M  
 APPLICANT: Lemieux, Sebastien M  
 TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and  
 FILE REFERENCE: 10182-018-999  
 CURRENT FILING DATE: 2002-04-23  
 PRIOR APPLICATION NUMBER: US/10/128,714  
 PRIOR FILING DATE: 2002-04-23  
 PRIOR APPLICATION NUMBER: US 60/285,697  
 PRIOR FILING DATE: 2001-04-23  
 PRIOR APPLICATION NUMBER: US 60/287,066  
 PRIOR FILING DATE: 2001-04-27  
 PRIOR APPLICATION NUMBER: US 60/295,890  
 PRIOR FILING DATE: 2001-06-05  
 PRIOR APPLICATION NUMBER: US 60/303,899  
 PRIOR FILING DATE: 2001-07-09  
 PRIOR APPLICATION NUMBER: US 60/316,362  
 PRIOR FILING DATE: 2001-08-31  
 NUMBER OF SEQ ID NOS: 8603  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 8338  
 LENGTH: 308  
 TYPE: PRT  
 ORGANISM: *Aspergillus fumigatus*  
 US-10-128-714-8338

Query Match 47.8%; Score 737; DB 15; Length 308;  
 Best Local Similarity 51.7%; Pred. No. 2.1e-70;  
 Matches 154; Conservative 47; Mismatches 85; Indels 12; Gaps 6;



```

Oy 7 SPAKDFLAGIAAISTAVAPIERVKLLLOYHASKOIAA--DKOYGIYDCIWRIPK 63
Db 7 APTDSFVAVGVSAVSKTAAPIERIKLL--VONODEMIRAGRLDRKTYNGIIDCFRRTAQ 64
Oy 64 BOGVLSPWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFMWRYFAGNLASGGAA 123
Db 65 AEGVMSLWRGNLANVIRYFPTQALNFAFRDLYKSMFAYKDR-DGYAKMMGNLASGGAA 123
Oy 124 GATSLCFYYPIDFARTLAADV--GKSGTEREFRLGDCLVKITYSDGIRGLYOGFSVSV 181
Db 124 GATSLLPFYSLDYARTLANDAKSAKGGGERQFNGLIDYRKTLASDGIAGLYRGFGPSV 183
Oy 182 OGIIYRAAYFGVYDTAKG-MLPDPKXTHIVSWMIAGTVTAVAGVSYPPEDTVRRMM 240
Db 184 LGIVVYRGLYFGMDSIKPVVLVGSLEGSFLASFLIGMTVTTGAGIASYPLDTIRRRMM 243
Oy 241 QSGRKGADIMYTGVCWRKIFRDEGKAFKFGAMSNVLRGMGAFVLVLYDELKVI 298
Db 244 TSGBA--VKYKSSLDARQIIRAKEGVKSLFKGAGANTLRGVAGAGVLSYDQVQLL 298

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Search completed: December 18, 2003, 12:55:44  
 Job time : 25.3606 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:46 ; Search time 14.3494 Seconds  
(without alignments)  
1997.178 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543  
Sequence: 1 MTEGAISFADFLAGTIAA.....LRGNGAFVLYVDELKKVI 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1	ADP,ATP carrier pr
2	1512	98.0	298	1	ADP,ATP carrier pr
3	1454	94.2	298	1	ADP,ATP carrier pr
4	1424	92.3	298	1	adenine nucleotide
5	1422	92.2	298	1	ADP,ATP carrier pr
6	1418	91.9	298	2	ADP,ATP carrier pr
7	1409	91.3	298	1	ADP,ATP carrier pr
8	1405	91.1	298	2	ADP,ATP carrier pr
9	1184	76.7	301	1	ADP,ATP carrier pr
10	1041	67.5	313	2	ADP,ATP carrier pr
11	1039	67.3	313	2	ADP,ATP carrier pr
12	1038	67.3	300	2	ADP,ATP carrier pr
13	993.5	64.4	300	2	ADP,ATP carrier pr
14	943	63.4	339	2	ADP,ATP carrier pr
15	943	61.1	301	2	ADP,ATP carrier pr
16	778.5	50.5	307	2	ADP,ATP carrier pr
17	772	50.0	308	1	ADP,ATP carrier pr
18	769	49.8	322	2	ADP,ATP carrier pr
19	768	49.8	386	2	ADP,ATP carrier pr
20	766	49.6	313	1	ADP,ATP carrier pr
21	764	49.5	326	2	ADP,ATP carrier pr
22	762.5	49.4	305	2	ADP,ATP carrier pr
23	760.5	49.3	318	1	ADP,ATP carrier pr
24	756.5	49.0	306	2	ADP,ATP carrier pr
25	750	48.6	387	2	ADP,ATP carrier pr
26	748	48.5	386	2	ADP,ATP carrier pr
27	747	48.4	306	2	ADP,ATP carrier pr
28	747	48.4	386	2	ADP,ATP carrier pr
29	744	48.2	387	2	ADP,ATP carrier pr

30	743	48.2	379	2	ADP,ATP carrier pr
31	742.5	48.1	385	1	ADP,ATP carrier pr
32	742	48.1	382	2	ADP,ATP carrier pr
33	739.5	47.9	386	2	ADP,ATP carrier pr
34	737.5	47.8	309	2	ADP,ATP carrier pr
35	734.5	47.6	379	2	ADP,ATP carrier pr
36	681.5	44.2	298	2	ADP,ATP carrier pr
37	520.5	33.7	327	2	ADP,ATP carrier pr
38	383	24.8	325	2	ADP,ATP carrier pr
39	381	24.7	352	2	ADP,ATP carrier pr
40	372	24.1	358	2	ADP,ATP carrier pr
41	370.5	24.0	415	2	ADP,ATP carrier pr
42	369.5	23.9	381	2	ADP,ATP carrier pr
43	368	23.8	475	2	ADP,ATP carrier pr
44	363	23.5	348	2	ADP,ATP carrier pr
45	344.5	22.3	332	2	ADP,ATP carrier pr

## ALIGNMENTS

## RESULT 1

ADP,ATP carrier protein T3 - human  
N/Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,ATP  
C/Species: Homo sapiens (man)  
C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
C/Accession: S03894; B28116  
R/Cozens, A.L., Runswick, M.J., Walker, J.E.  
J. Mol. Biol. 206, 261-280, 1989  
A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP  
A/Reference number: S03893; MUID:69236396; PMID:2541251  
A/Accession: S03894  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-298 <CO2>  
R/Houldsworth, J., Attardi, G.  
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
A/Reference number: A94197; MUID:88124845; PMID:2829183  
A/Accession: B28116  
A/Molecule type: mRNA  
A/Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>  
A/Cross-references: GB:J03552; NID:g339722; PIDD:AAA36750.1; PID:g339723  
A/Experimental source: liver  
C/Genetics:  
A/Gene: GDB:ANT3; ANT3Y  
A/Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3  
A/Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:  
C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
F/2-298/Product: ADP,ATP carrier protein #status predicted <MAT>  
F/5-99/Domains: ADP,ATP carrier protein repeat homology <ACP1>  
F/110-202/Domains: ADP,ATP carrier protein repeat homology <ACP2>  
F/207-298/Domains: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 6e-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTEGAISFADFLAGTIAAISKTAIVPIRKYLLLOVQASKOIADKQYKIVDCIVR	60
Db	1	MTEGAISFADFLAGTIAAISKTAIVPIRKYLLLOVQASKOIADKQYKIVDCIVR	60
Qy	61	IPKQGVLSFMRGNLAVIYFPPTQALNPAFKQYKQIFGQVYKHQFMRYPFAGNLASG	120
Db	61	IPKQGVLSFMRGNLAVIYFPPTQALNPAFKQYKQIFGQVYKHQFMRYPFAGNLASG	120
Qy	121	GAAGATSLCFVYPLDFARTLADVQKSGTEREPRGIGDCLVTKTSGDGRIGLYQGSFVS	180
Db	121	GAAGATSLCFVYPLDFARTLADVQKSGTEREPRGIGDCLVTKTSGDGRIGLYQGSFVS	180

QY 181 VGGIITTYAAYFGVDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPTTVRRMM 240  
 |||||  
 DB 181 VGGIITTYAAYFGVDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPTTVRRMM 240  
 |||||  
 QY 241 OSGRKADIMTYGTVDCKWKIRFDEGKAFKFGANSNVLKRGGAFLVLYDELKKVI 298  
 |||||  
 DB 241 OSGRKADIMTYGTVDCKWKIRFDEGKAFKFGANSNVLKRGGAFLVLYDELKKVI 298  
 |||||

## RESULT 2

B43646  
 ADP, ATP carrier protein T2 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 20-Aug-1999  
 C:Accession: B43646  
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.  
 Biochemistry 28, 866-873, 1989

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
 A:Reference number: A43646; MUID:89229093; PMID:2540808

A:Accession: B43646

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <POM>

A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417  
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;  
 Best Local Similarity 97.7%; Pred. No. 3, 3e-126;

Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHSKQIADKQYGIYDCIVR 60  
 |||||  
 DB 1 MTEQAIISPAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHSKQIADKQYGIYDCIVR 60  
 |||||  
 QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPFAGNLASG 120  
 |||||  
 DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPFAGNLASG 120  
 |||||  
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTERBFRGLDCLVKYTKSDGIRGLYQGFVS 180  
 |||||  
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTERBFRGLDCLVKYTKSDGIRGLYQGFVS 180  
 |||||  
 QY 181 VGGIITTYAAYFGVDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPTTVRRMM 240  
 |||||  
 DB 181 VGGIITTYAAYFGVDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPTTVRRMM 240  
 |||||  
 QY 241 OSGRKADIMTYGTVDCKWKIRFDEGKAFKFGANSNVLKRGGAFLVLYDELKKVI 298  
 |||||  
 DB 241 OSGRKADIMTYGTVDCKWKIRFDEGKAFKFGANSNVLKRGGAFLVLYDELKKVI 298  
 |||||

## RESULT 3

A29132  
 ADP, ATP carrier protein T2 - human

N:Alternate names: mitochondrial ADP, ATP translocase 2

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000

C:Accession: A29132; C28116

R:Barclay, R.; Ferrarini, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.

J. Biol. Chem. 262, 4355-4359, 1987

A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat

A:Reference number: A29132; MUID:87166056; PMID:3031073

A:Accession: A29132

A:Molecule type: mRNA

A:Residues: 1-298 <BAT>

A:Cross-references: GB:J02683; NID:9179246; PIDN:AAA5579.1; PID:9179247

R:Holdsworth, J.; Atterdill, G. 85, 377-381, 1988

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: C28116

A:Molecule type: mRNA

A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>

A:Cross-references: GB:J03591; NID:9339720; PIDN:AAA36749.1; PID:9339721

A:Experimental source: clone PHAT3

C:Genetics:

A:Gene: GDB:AMT2; T3; 2P1

A:Cross-references: GDB:125190; OMIM:300150

A:Map position: Xq13-Xq26

A:Note: there may be some confusion in the assignment of sequences for GDB:AMT2 and GDB:

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 4, 5e-121;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHSKQIADKQYGIYDCIVR 60  
 |||||  
 DB 1 MTEQAIISPAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHSKQIADKQYGIYDCIVR 60  
 |||||  
 QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPFAGNLASG 120  
 |||||  
 DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPFAGNLASG 120  
 |||||  
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTERBFRGLDCLVKYTKSDGIRGLYQGFVS 180  
 |||||  
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTERBFRGLDCLVKYTKSDGIRGLYQGFVS 180  
 |||||  
 QY 181 VGGIITTYAAYFGVDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPTTVRRMM 240  
 |||||  
 DB 181 VGGIITTYAAYFGVDTAKGMLPDPKNTHTIVSNMIAQTVTAAGVSVPTTVRRMM 240  
 |||||  
 QY 241 OSGRKADIMTYGTVDCKWKIRFDEGKAFKFGANSNVLKRGGAFLVLYDELKK 296  
 |||||  
 DB 241 OSGRKADIMTYGTVDCKWKIRFDEGKAFKFGANSNVLKRGGAFLVLYDELKK 296  
 |||||

## RESULT 4

I60173  
 adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999

C:Accession: I60173

R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

Biochim. Biophys. Acta 1152, 192-196, 1993

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A:Reference number: I60173; MUID:94002161; PMID:8399300

A:Accession: I60173

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 <RES>

A:Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA3842.1; PID:9400427

C:Genetics:

A:Gene: anti

A:Introns: 37/3; 200/1; 247/1

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;  
 Best Local Similarity 89.6%; Pred. No. 2e-118;

Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHSKQIADKQYGIYDCIVR 60  
 |||||  
 DB 1 MTEQAIISPAKDFLAGGIAAISTKTAIVAPIERVKLLQVQHSKQIADKQYGIYDCIVR 60  
 |||||

QY 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 Db 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPFATRLAADVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPLDPFATRLAADVGKSGSERFNGLDCLTKIFKSDGLKGLYOGFSVS 180  
 QY 181 VGGIITRYAAVFGVYDTRAKGMLPDPKNTHTIVSNMIAQCTVTAAGVVSYPPTVRRMM 240  
 Db 181 VGGIITRYAAVFGVYDTRAKGMLPDPKNTHTIVSNMIAQSVTAAGVVSYPPTVRRMM 240  
 QY 241 OSGRKADIMVTGTVDCKRKIFRDEGKAFPKGAMSNVLRMGCAFVLYLDELKCVI 298  
 Db 241 OSGRKADIMVTGTVDCKRKIKADGKRAFFKGMNSVLRMGCAFVLYLDELKCVI 298

## RESULT 5

KWBO  
 ADP, ATP carrier protein T1 - bovine  
 N/Alternate names: ADP/ATP translocase T1  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 14-Nov-1983 #sequence revision 22-Jul-1994 #text\_change 22-Jun-1999  
 C/Accession: A43646; A24822; A03181; A61343; S69369  
 R/Powell, S.J.; Mead, S.M.; Runswick, M.J.; Walker, J.E.  
 Biochemistry 28, 866-873, 1989  
 A/Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
 A/Reference number: A43646; MUID:89229093; PMID:2540808  
 A/Accession: A43646  
 A/Molecule type: mRNA  
 A/Residues: 1-298 <POW>  
 A/Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415  
 R/Rasmussen, U.B.; Wolfrum, H.  
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986  
 A/Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual  
 A/Reference number: A24822; MUID:86295775; PMID:3017341  
 A/Accession: A24822  
 A/Molecule type: mRNA  
 A/Residues: 208-298 <RAS>  
 A/Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631  
 R/Aquila, H.; Maser, D.; Bulitz, M.; Klingenberg, M.  
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982  
 A/Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria  
 A/Reference number: A03181; MUID:82188267; PMID:7076130  
 A/Accession: A03181  
 A/Molecule type: protein  
 A/Residues: 2-51, 'X', '53-70', 'X', '72-109', 'X', '111-298 <AGU>  
 A/Note: residue 52 may be methyllysine  
 R/Babel, W.; Wachter, B.; Aquila, H.; Klingenberg, M.  
 Biochim. Biophys. Acta 670, 176-180, 1981  
 A/Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitoch  
 A/Reference number: A61343; MUID:82046808; PMID:6271240  
 A/Accession: A61343  
 A/Molecule type: protein  
 A/Residues: 205-298 <BAB>  
 R/Oettermeyer, W.; Mason, K.; Kalima, S.  
 Eur. J. Biochem. 227, 730-733, 1995  
 A/Title: [(3)H]-7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP  
 A/Reference number: S69369; MUID:95172058; PMID:7867632  
 A/Accession: S69369  
 A/Molecule type: protein  
 A/Residues: 49-63;154-168 <OET>  
 A/Comment: This protein is synthesized in the cytosol and transported into the mitochond  
 C/Complex: homodimer  
 C/Function:  
 A/Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera  
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C/Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch  
 F/5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
 F/110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
 F/207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

F/2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental  
 F/52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;  
 Best Local Similarity 89.3%; Pred. No. 3.1e-118;  
 Matches 266; Conservative 19; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 MTEQALSPKQFLAGGIAAISTKAVAPIREVKLLIQVHASKQIADKQKGYDCTVR 60  
 Db 1 MSDQALSTLPKQFLAGGAAISTKAVAPIREVKLLIQVHASKQISAEKQYKGIIDCVVR 60  
 QY 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 Db 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPFATRLAADVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPLDPFATRLAADVGKSGSERFNGLDCLTKIFKSDGLKGLYOGFSVS 180  
 QY 181 VGGIITRYAAVFGVYDTRAKGMLPDPKNTHTIVSNMIAQCTVTAAGVVSYPPTVRRMM 240  
 Db 181 VGGIITRYAAVFGVYDTRAKGMLPDPKNTHTIVSNMIAQSVTAAGVVSYPPTVRRMM 240  
 QY 241 OSGRKADIMVTGTVDCKRKIFRDEGKAFPKGAMSNVLRMGCAFVLYLDELKCVI 298  
 Db 241 OSGRKADIMVTGTVDCKRKIKADGKRAFFKGMNSVLRMGCAFVLYLDELKCVI 298

## RESULT 6

S37210  
 ADP, ATP carrier protein T1 - mouse  
 N/Alternate names: adenine nucleotide carrier  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text\_change 20-Aug-1999  
 C/Accession: S37210  
 R/Laplace, C.; Cochet, P.  
 submitted to the EMBL Data Library, September 1993  
 A/Reference number: S37210  
 A/Accession: S37210  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-298 <LAP>  
 A/Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628  
 C/Genetic: ANCI  
 A/Gene: ANCI  
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C/Keywords: duplication; transmembrane protein  
 F/5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
 F/110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
 F/207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>  
 Query Match 91.9%; Score 1418; DB 2; Length 298;  
 Best Local Similarity 88.9%; Pred. No. 6.9e-118;  
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 MTEQALSPKQFLAGGIAAISTKAVAPIREVKLLIQVHASKQIADKQKGYDCTVR 60  
 Db 1 MGDQALSTLPKQFLAGGIAAISTKAVAPIREVKLLIQVHASKQISAEKQYKGIIDCVVR 60  
 QY 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 Db 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPFATRLAADVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPLDPFATRLAADVGKSGSERFNGLDCLTKIFKSDGLKGLYOGFSVS 180  
 QY 181 VGGIITRYAAVFGVYDTRAKGMLPDPKNTHTIVSNMIAQCTVTAAGVVSYPPTVRRMM 240  
 Db 181 VGGIITRYAAVFGVYDTRAKGMLPDPKNTHTIVSNMIAQSVTAAGVVSYPPTVRRMM 240  
 QY 241 OSGRKADIMVTGTVDCKRKIFRDEGKAFPKGAMSNVLRMGCAFVLYLDELKCVI 298  
 Db 241 OSGRKADIMVTGTVDCKRKIKADGKRAFFKGMNSVLRMGCAFVLYLDELKCVI 298

Db 241 QSGRKGADIMTGTGTCCKRIAKDEGANAFFKGAANSVLRGMGAFVLVDEIKYV 298

## RESULT 7

ADP/ATP carrier protein T1 - human  
 N/Alternate names: mitochondrial ADP/ATP translocase 1  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C/Accession: A44778; S03893; A39891; A28116  
 R/Li: K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.  
 J. Biol. Chem. 264, 13998-14004, 1999  
 A/Title: A human muscle adenine nucleotide translocator gene has four exons, is located  
 A/Reference number: A44778; MUID:89340499; PMID:2547778  
 A/Accession: A44778  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-298 <LTA>  
 A/Cross-references: GB:J04982; NID:9178658; PIDN:AAA51736.1; PID:9178659  
 R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.  
 J. Mol. Biol. 206, 261-280, 1989  
 A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr  
 A/Reference number: S03893; MUID:8936396; PMID:2541251  
 A/Accession: S03893  
 A/Status: not compared with conceptual translation  
 A/Molecule type: DNA  
 A/Residues: 1-298 <COZ>  
 R/Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987  
 A/Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader  
 A/Reference number: A39891; MUID:88041149; PMID:2832266  
 A/Accession: A39891  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>  
 A/Cross-references: GB:J02966; NID:933919; PIDN:AAA61223.1; PID:933920  
 A/Experimental source: clone PHMANT  
 R/Houldsworth, J.; Altardi, G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
 A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
 A/Reference number: A4197; MUID:88124845; PMID:2829183  
 A/Accession: A28116  
 A/Molecule type: mRNA  
 A/Residues: 1-37 <HOU>  
 A/Cross-references: GB:J03593; NID:9339724; PIDN:AAA6751.1; PID:9339725  
 A/Experimental source: liver  
 C/Genetics:  
 A/Genes: GDB:ANT1, T1  
 A/Cross-references: GDB:119680; OMIM:103220  
 A/Map position: 4q35-4q35  
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F/2-298/Product: ADP/ATP carrier protein status predicted <MNT>  
 F/5-99/Domains: ADP/ATP carrier protein repeat homology <ACPI>  
 F/110-202/Domains: ADP/ATP carrier protein repeat homology <ACP2>  
 F/207-298/Domains: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.3%; Score 1409; DB 1; Length 298;  
 Best Local Similarity 88.3%; Pred. No. 4.3e-117;  
 Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTEQASFAKDFLAGGIAAASKTAVAPIERVKLLIQVQHASKOIAADKQYKGYVDCYR 60  
 Db 1 MGDHMSFLKDFLAGGVAASKTAVAPIERVKLLIQVQHASKOISAEKQYKGIIDCYR 60

Qy 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVGHQTFMRYFAGNLASG 120  
 Db 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVGHQTFMRYFAGNLASG 120

Qy 121 GAAGTSTCFYYPDPFATRLAADVGKSGTERRFGGLDCKVTKRSGIRGLYQSGFSVS 180  
 Db 121 GAAGTSTCFYYPDPFATRLAADVGKGAORHFGGLDCKVTKRSGIRGLYQSGFVS 180

Qy 181 VGGIITTAAYFGYVDTKXGMLPDPKXTHIVVSMIAQTYTAVAGVSPFDTVRRMM 240  
 Db 181 VGGIITTAAYFGYVDTKXGMLPDPKXTHIVVSMIAQSYTAVAGLVSPFDTVRRMM 240

Qy 241 QSGRKGADIMTGTGTCCKRIAFDEGKAFKFGKAMSNTLRGMGAFVLVDEIKYV 298  
 Db 241 QSGRKGADIMTGTGTCCKRIAKDEGANAFFKGAANSVLRGMGAFVLVDEIKYV 298

## RESULT 8

ADP/ATP carrier protein T2 - mouse  
 N/Alternate names: adenine nucleotide translocase  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Apr-1998  
 C/Accession: S31814  
 R/Coates, P.; Laplace, C.  
 submitted to the EMBL Data Library, January 1993  
 A/Reference number: S31814  
 A/Accession: S31814  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-298 <COS>  
 A/Cross-references: EMBL:X70847  
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C/Keywords: duplication; transmembrane protein  
 F/5-99/Domains: ADP/ATP carrier protein repeat homology <ACP1>  
 F/110-202/Domains: ADP/ATP carrier protein repeat homology <ACP>  
 F/207-298/Domains: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.1%; Score 1405; DB 2; Length 298;  
 Best Local Similarity 89.2%; Pred. No. 9.8e-117;  
 Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTEQASFAKDFLAGGIAAASKTAVAPIERVKLLIQVQHASKOIAADKQYKGYVDCYR 60  
 Db 1 MTDNAVSFAKDFLAGGVAASKTAVAPIERVKLLIQVQHASKOITADKQYKGIIDCYR 60

Qy 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVGHQTFMRYFAGNLASG 120  
 Db 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDVGHQTFMRYFAGNLASG 120

Qy 121 GAAGTSTCFYYPDPFATRLAADVGKSGTERRFGGLDCKVTKRSGIRGLYQSGFSVS 180  
 Db 121 GAAGTSTCFYYPDPFATRLAADVGKGAERERGLDCKVTKYSGIRGLYQSGFVS 180

Qy 181 VGGIITTAAYFGYVDTKXGMLPDPKXTHIVVSMIAQTYTAVAGVSPFDTVRRMM 240  
 Db 181 VGGIITTAAYFGYVDTKXGMLPDPKXTHIVVSMIAQSYTAVAGLVSPFDTVRRMM 240

Qy 241 QSGRKGADIMTGTGTCCKRIAFDEGKAFKFGKAMSNTLRGMGAFVLVDEIKYV 296  
 Db 241 QSGRKGADIMTGTGTCCKRIARDEGKAFKFGKAMSNTLRGMGAFVLVDEIKYV 296

## RESULT 9

ADP/ATP carrier protein - African malaria mosquito  
 C/Species: Anopheles gambiae (African malaria mosquito)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: S31935; S31936  
 R/Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.  
 submitted to the EMBL Data Library, February 1993  
 A/Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.  
 A/Reference number: S31935  
 A/Accession: S31935  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-301 <BEA>  
 A/Cross-references: EMBL:Z21814; EMBL:Z21815  
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C/Keywords: duplication; transmembrane protein  
 F/7-101/Domains: ADP/ATP carrier protein repeat homology <ACP1>

F:112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F:209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 76.7%; Score 1184; DB 1; Length 301;  
Best Local Similarity 77.0%; Pred. No. 3.6e-97;  
Matches 231; Conservative 23; Mismatches 44; Indels 2; Gaps 1;

QY 1 MTEQA--ISPAKDLAAGIAAISTKAVAPIERVKLLQVHASKQIADKQYGIYDCI 58  
DB 1 MTKKADPRGPAKDLAAGIAAISTKAVAPIERVKLLQVHASKQIADKQYGIYDCI 60  
QY 59 VRIPKEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIPLGVDKTKQFMRYPAGNTA 118  
DB 61 VRIPKEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIPLGVDKTKQFMRYPAGNTA 120  
QY 119 SGGAAGATSLCFYVPLDPARTRLADVGKSTGEREFGDCLVKTSGKIGLYQGSVSVOGIIIT 178  
DB 121 SGGAAGATSLCFYVPLDPARTRLADVGKSTGEREFGDCLVKTSGKIGLYQGSVSVOGIIIT 180  
QY 179 VSVGGIITIRAAVGVYDTAKGMLPDPKNTIIVSWMLAQVTAVAGVSVPTVRRM 238  
DB 181 VSVGGIITIRAAVGVYDTAKGMLPDPKNTIIVSWMLAQVTAVAGVSVPTVRRM 240  
QY 239 MMQSGRKADIMYTGVDCKWKRIFRDEGKAPFKGAMSNVLRGKGAFVLVLYDELKXVI 298  
DB 241 MMQSGRKADIMYTGVDCKWKRIFRDEGKAPFKGAMSNVLRGKGAFVLVLYDELKXVI 300

## RESULT 10

123207  
hypothetical protein K01H12.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C:Accession: T23207

R:McMurray, A.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: Z19707  
A:Accession: T23207  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-313 <W1>  
A:Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2  
A:Experimental source: clone K01H12  
C:Genetics:  
A:Gene: CESP:K01H12.2  
A:Map position: 4  
A:Intons: 4/1; 191/2  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.5%; Score 1041; DB 2; Length 313;  
Best Local Similarity 70.9%; Pred. No. 1.7e-84;  
Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDPLAGIAAISTKAVAPIERVKLLQVHASKQIADKQYGIYDCIIRIPKEQV 67  
DB 25 FLIDLAGGTAAASKTAVAPIERVKLLQVHASKQIADKQYGIYDCIIRIPKEQV 84  
QY 68 LSPFRGNLANVIRYPTQALNFAFKDKYKQIPLGVDKTKQFMRYPAGNTASGGAAGATS 127  
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIPLGVDKTKQFMRYPAGNTASGGAAGATS 144  
QY 128 LCFYVPLDPARTRLADVGKSTGEREFGDCLVKTSGKIGLYQGSVSVOGIIIT 187  
DB 145 LCFYVPLDPARTRLADVGKSTGEREFGDCLVKTSGKIGLYQGSVSVOGIIIT 203  
QY 188 RAAVGVYDTAKGMLPDPKNTIIVSWMLAQVTAVAGVSVPTVRRMMSQGRK 246  
DB 204 RAAVGVYDTAKGMLPDPKNTIIVSWMLAQVTAVAGVSVPTVRRMMSQGRK 262  
QY 247 ADIMYTGVDCKWKRIFRDEGKAPFKGAMSNVLRGKGAFVLVLYDELKXVI 298  
DB 263 -DVLVYKNTLDCAVKIKNEGMSAMFKGALSIVFRGTGALVLAIDYDIQKFI 313

## RESULT 11

125850  
hypothetical protein T01B11.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C:Accession: T25850

R:Geisel, C./Stelljes, L.  
submitted to the EMBL Data Library, December 1996  
A:Description: The sequence of C. elegans cosmid T01B11.  
A:Reference number: Z20099  
A:Accession: T25850  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-313 <GB1>  
A:Cross-references: EMBL:U80931; PIDN:AB38001.1; GSPDB:GN00022; CESP:T01B11.4  
A:Experimental source: strain Bristol N2; clone T01B11  
C:Genetics:  
A:Gene: CESP:T01B11.4  
A:Map position: 4  
A:Intons: 4/1; 191/2  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1039; DB 2; Length 313;  
Best Local Similarity 70.9%; Pred. No. 2.6e-84;  
Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDPLAGIAAISTKAVAPIERVKLLQVHASKQIADKQYGIYDCIIRIPKEQV 67  
DB 25 FLIDLAGGTAAASKTAVAPIERVKLLQVHASKQIADKQYGIYDCIIRIPKEQV 84  
QY 68 LSPFRGNLANVIRYPTQALNFAFKDKYKQIPLGVDKTKQFMRYPAGNTASGGAAGATS 127  
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIPLGVDKTKQFMRYPAGNTASGGAAGATS 144  
QY 128 LCFYVPLDPARTRLADVGKSTGEREFGDCLVKTSGKIGLYQGSVSVOGIIIT 187  
DB 145 LCFYVPLDPARTRLADVGKSTGEREFGDCLVKTSGKIGLYQGSVSVOGIIIT 203  
QY 188 RAAVGVYDTAKGMLPDPKNTIIVSWMLAQVTAVAGVSVPTVRRMMSQGRK 246  
DB 204 RAAVGVYDTAKGMLPDPKNTIIVSWMLAQVTAVAGVSVPTVRRMMSQGRK 262  
QY 247 ADIMYTGVDCKWKRIFRDEGKAPFKGAMSNVLRGKGAFVLVLYDELKXVI 298  
DB 263 -DVLVYKNTLDCAVKIKNEGMSAMFKGALSIVFRGTGALVLAIDYDIQKFI 313

## RESULT 12

125371  
hypothetical protein T27B9.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C:Accession: T25371

R:Lloyd, C.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z20024  
A:Accession: T25371  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-300 <W1>  
A:Cross-references: EMBL:Z82059; PIDN:CA804874.1; GSPDB:GN00021; CESP:T27B9.1  
A:Experimental source: clone T27B9  
C:Genetics:  
A:Gene: CESP:T27B9.1  
A:Map position: 3  
A:Intons: 20/1; 41/3; 115/2  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1038; DB 2; Length 300;  
Best Local Similarity 69.2%; Pred. No. 3e-84;  
Matches 202; Conservative 37; Mismatches 49; Indels 4; Gaps 3;





```

Db      8 NPAADFLMGISAAISKTVTPPIERVKMLIOTODSIPEIKSQOVERYSGLINCFRRVSKE 67
Qy      65 QGVLSFMRGNLANVIRYFPTQALNFAFKDKYQIFLGVDKHTOPFWRYPAGNLASGAAG 124
        68 QGVLSLMKGNVANVIRIFPTQAFNFAFKDYFNKIF-PRYDQNTDPSKFCVNLISGATAG 126
Db      125 ATSLCFVYPLDPARTRLADVKGSGTEREFRLGDLVKITKSDGIRGLYOGFSYSVOGI 184
        127 AHSILIVYPLDPARTRLASDICK-GKDRQFTGLFDCLAKIKYQIGLISYSGFVSVTGI 185
Qy      185 IYRAAYFGVDTAKGML-PDPKXTHIVSWMIAQVTAVAGVSPFDTVRRRMMOSG 243
        186 IYRGSYFGLYDSAKALLFTNDKNTNIVLKNVAOSVTILAGLISYFPDTVRRRMMMSG 245
Qy      244 RKG-ADIMYTGVDCKRIFRDEGKAFPKGMSNVLRGMGAFTLVLYDELKXKI 298
        246 RKGKEIQKNTIDCMIKILRNEGFKFPKGAMANVIRGAGGALVLFYDELQKLI 301

```

Search completed: December 18, 2003, 12:44:05  
 Job time : 15.3494 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:01 ; Search time 30.701 Seconds

(without alignments)  
2504.793 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543  
Sequence: 1 MTEBAISPADFLAGIAA.....LRGGAFLVLYDELKKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL 23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriopl:\*

17: sp\_archaeopl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1474	95.5	298	13	Q8AYM3 Q8aym3 gallus galli
2	1451	94.0	298	6	Q8SOH5 Q8soh5 bos taurus
3	1446	93.7	298	13	Q8JHI0 Q8jhi0 brachydanio
4	1422	92.2	298	6	O46373 O46373 oycetolagus
5	1421	92.1	298	13	Q919W9 Q919w9 xenopus lae
6	1414	91.6	298	11	Q8BV19 Q8bv19 mus musculus
7	1409	91.3	298	13	Q9PR11 Q9pr11 rana rugosa
8	1406	91.1	298	13	Q9PR12 Q9pr12 rana rugosa
9	1402	90.9	298	13	Q9YIC4 Q9yic4 rana rugosa
10	1300	84.3	299	5	Q8SVY4 Q8svy4 ethiostigm
11	1259	81.6	317	13	Q91336 Q91336 rana sylvat
12	1254.5	81.3	312	5	Q8IRAO Q8irao drosophila
13	1235.5	80.1	300	5	Q9NHWS Q9nhws lucilia cup
14	1187.5	77.0	288	5	O44093 O44093 drosophila
15	1183.5	76.7	288	5	O44094 O44094 drosophila
16	1176.5	76.2	304	5	Q25129 Q25129 halocynthia

17	1159	75.1	254	11	Q8BK05 Q8bk05 mus musculus
18	1137.5	73.7	307	5	O62526 O62526 drosophila
19	1119	72.5	315	4	Q9H0C2 Q9h0c2 homo sapien
20	1041	67.5	313	5	Q21103 Q21103 caenorhabdi
21	1039	67.3	313	5	P91410 P91410 caenorhabdi
22	1038	67.3	300	5	O45865 O45865 caenorhabdi
23	1036.5	67.2	310	10	O8H727 O8h727 phycophor
24	996	64.5	309	5	O97470 O97470 dictyosteli
25	993.5	64.4	300	5	O01813 O01813 caenorhabdi
26	993	64.4	300	5	O17407 O17407 caenorhabdi
27	973.5	63.1	318	5	Q9BJ36 Q9bj36 toxoplasma
28	947	61.4	301	5	O81J34 O81j34 plasmodium
29	946.5	61.3	307	8	O9XM22 O9xm22 ascaris suu
30	944	61.2	301	5	O25692 O25692 plasmodium
31	944	61.2	301	5	Q8MYR4 Q8myr4 eplotes sp
32	943	61.1	301	5	Q26006 Q26006 plasmodium
33	936	60.7	305	5	Q8MYR7 Q8myr7 nyctotherus
34	932	60.4	308	5	Q8MYR8 Q8myr8 nyctotherus
35	924	59.9	306	5	Q8MYR5 Q8myr5 nyctotherus
36	924	59.9	308	5	Q8MYR6 Q8myr6 nyctotherus
37	827	53.6	170	6	Q9X869 Q9x869 sus scrofa
38	778.5	50.5	305	3	Q9P8M1 Q9p8m1 yarrowia li
39	767.5	49.7	302	3	Q8J0M2 Q8j0m2 yarrowia li
40	764	49.5	326	5	P91270 P91270 caenorhabdi
41	760	49.3	307	5	O76286 O76286 trypanosoma
42	759	49.2	303	3	O74260 O74260 candida par
43	756.5	49.0	306	5	Q18683 Q18683 caenorhabdi
44	753	48.8	307	5	Q26697 Q26697 trypanosoma
45	749	48.5	315	3	O8J0U1 O8j0u1 gaeananomy

## ALIGNMENTS

## RESULT 1

ID Q8AYM3 PRELIMINARY; PRT; 298 AA.

AC Q8AYM3; (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE ATP/ADP antiporter.

GN AVANT.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.,

RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP

RL FEBS Lett. 0:0-0(2002).

DR EMBL, AB088686; BAC1553.1; -

SQ SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;

Query Match 95.5%; Score 1474; DB 13; Length 298;

Best Local Similarity 93.0%; Pred. No. 2.5e-125;

Matches 277; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTEBAISPADFLAGIAAISKTAVPRIERVKLLVQHASKOIADKQKIVDCIVR 60

DB 1 MADDAISFLDPLFARGVAAISKTAVPRIERVKLLVQHASKOIADKQKIVDCIVR 60

QY 61 IPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKHOQFMRYPAGNLASG 120

DB 61 IPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKHOQFMRYPAGNLASG 120

QY 121 GAAGATSLCFVYPLDPAFRTIADLVGKSGTERBERFGVDCLVKTKSGIRGLVQGSFVS 180

DB 121 GAAGATSLCFVYPLDPAFRTIADLVGKSGTERBERFGVDCLVKTKSGIRGLVQGSFVS 180

QY 181 VGGIITRAAYFGVYDPAKGLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240  
 DB 181 VGGIITRAAYFGVYDPAKGLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240  
 QY 241 QSGRKGADIMTGTVDCKRKIFRDEGGAFFKAGMSNTLRGMAFVLYLDELKVI 298  
 DB 241 QSGRKGADIMTGTVDCKRKIFRDEGGAFFKAGMSNTLRGMAFVLYLDELKVI 298

## RESULT 2

Q8SCH5 PRELIMINARY; PRT; 298 AA.

AC Q8SCH5  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Adenine nucleotide translocator 2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamazaki N., Shiohara Y., Tanida K., Terada H.;  
 RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:  
 RT identification of possible amino acids that determine functional  
 RT differences in its isoforms."  
 RL Mitochondrion 1:371-379(2002).  
 DR EMBL; AB065433; BAB84673.1;  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carrier.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 94.0%; Score 1451; DB 6; Length 298;

Best Local Similarity 92.2%; Pred. No. 3e-123;

Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKQITADKQYKGIYDCTVR 60  
 DB 1 MTEQAISPAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKQITADKQYKGIYDCTVR 60  
 QY 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120  
 DB 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120  
 QY 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDGLVKTGSDGIRGLYQGFVS 180  
 DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDGLVKTGSDGIRGLYQGFVS 180  
 QY 181 VGGIITRAAYFGVYDPAKGLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240  
 DB 181 VGGIITRAAYFGVYDPAKGLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240  
 QY 241 QSGRKGADIMTGTVDCKRKIFRDEGGAFFKAGMSNTLRGMAFVLYLDELKVI 298  
 DB 241 QSGRKGADIMTGTVDCKRKIFRDEGGAFFKAGMSNTLRGMAFVLYLDELKVI 298

## RESULT 3

Q8BHI0 PRELIMINARY; PRT; 298 AA.

AC Q8BHI0  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Solute carrier family 25 member 5 protein.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22035902; PubMed=12006978;  
 RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado B., Chen W.,  
 RA Burgess S., Hald M., Artzt K., Farrington S., Lin S.-Y., Nassen R.M.,  
 RA Hopkins N.;  
 RT "Insertional mutagenesis in zebrafish rapidly identifies genes  
 RT essential for early vertebrate development."  
 RL Nat. Genet. 31:135-140(2002).  
 DR EMBL; AF506216; AAM34660.1;  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carrier.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 SQ SEQUENCE 298 AA; 32763 MW; D78663CF5C51D39 CRC64;

Query Match 93.7%; Score 1446; DB 13; Length 298;

Best Local Similarity 91.9%; Pred. No. 8.5e-123;

Matches 274; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKQITADKQYKGIYDCTVR 60  
 DB 1 MTEQAISPAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKQITADKQYKGIYDCTVR 60  
 QY 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120  
 DB 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120  
 QY 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDGLVKTGSDGIRGLYQGFVS 180  
 DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDGLVKTGSDGIRGLYQGFVS 180  
 QY 181 VGGIITRAAYFGVYDPAKGLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240  
 DB 181 VGGIITRAAYFGVYDPAKGLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240  
 QY 241 QSGRKGADIMTGTVDCKRKIFRDEGGAFFKAGMSNTLRGMAFVLYLDELKVI 298  
 DB 241 QSGRKGADIMTGTVDCKRKIFRDEGGAFFKAGMSNTLRGMAFVLYLDELKVI 298

## RESULT 4

Q46373 PRELIMINARY; PRT; 298 AA.

AC Q46373  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skkeletal muscle;  
 RA Yamaguchi N., Kasai M.;  
 RT "Identification of a 30kDa calsequestrin-binding protein, which  
 RT regulates calcium release from sarcoplasmic reticulum of rabbit  
 RT skeletal muscle."  
 RL J. Biochem. 335:541-547(1998).  
 DR EMBL; AB009386; BAB23777.1;  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carrier.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH CARRIER; 3.  
KW Membrane; Transmembrane; Transport.  
SQ SEQUENCE 298 AA; 32901 MW; CAA832C088164AD78 CRC64;

Query Match 92.2%; Score 1422; DB 6; Length 298;  
Best Local Similarity 88.9%; Pred. No. 1.3e-120;  
Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

```
OY 1 MTEQAIISAKDPLAGGIAAISTKAVAPIERVKLLQVQHASKOIAADKOYGVDCIVR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSDQSLSTLKDPLAGGIAAASKTAVAPIERVKLLQVQHASKOISAKOYGIIDCVRR 60

OY 61 IPKEQGVLSFMRGNLANIYIRYPTQALNPAFKDKTKQIFLGVDKHTQFWRYPAGNLASG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEGGLISFMRGNLANIYIRYPTQALNPAFKDKTKQIFLGVDKHTQFWRYPAGNLASG 120

OY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVKTISDGINLQYGFVS 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYVPLDPARTRLAADVGKGAQREFGSLGNCLTKIFKSDGLRGLYGFVS 180

OY 181 VGGIIYRAAYFGVYDPAKGMPLDPKNTHIYVSNMIAQTVAVAGVSPPTVARRMM 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VGGIIYRAAYFGVYDPAKGMPLDPKNTHIYVSNMIAQTVAVAGVSPPTVARRMM 240

OY 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFFKGAWSNVLKMGAFVLVYDELKVI 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGVDCKRKIAKDEGAKAFKGAWSNVLKMGAFVLVYDELKVI 298
```

## RESULT 5

O919M9 PRELIMINARY; PRT; 298 AA.  
AC O919M9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Adenine nucleotide translocase.  
GN ANTL.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_Taxid=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Crawford M.J., Khosrowshanian F., Varmura S.L., Liverage R.A.;  
RT "Xenopus Adenine Nucleotide translocase mRNA Exhibits Specific and  
RT Dynamic Patterns of Expression During Development.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
DR EMBL; AF21347; AAF63471.1; -;  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR InterPro; IPR002067; Mlt\_carrier.  
DR InterPro; IPR002030; Mlt\_uncoupling.  
DR Pfam; PF00153; mito\_carr; 3.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PRINITS; PR00784; MTUNCOUPLING.  
DR PROSITE; PS00215; MITOCH CARRIER; 3.  
KW Membrane; Transmembrane; Transport.  
SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 92.1%; Score 1421; DB 13; Length 298;  
Best Local Similarity 90.3%; Pred. No. 1.6e-120;  
Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

```
OY 1 MTEQAIISAKDPLAGGIAAISTKAVAPIERVKLLQVQHASKOIAADKOYGVDCIVR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTDALISAKDPLAGGIAAISTKAVAPIERVKLLQVQHASKOITADKHKGINDCVRR 60

OY 61 IPKEQGVLSFMRGNLANIYIRYPTQALNPAFKDKTKQIFLGVDKHTQFWRYPAGNLASG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEGGLISFMRGNLANIYIRYPTQALNPAFKDKTKQIFLGVDKHTQFWRYPAGNLASG 120
```

```
OY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVKTISDGINLQYGFVS 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYVPLDPARTRLAADVGKANREPRGLDCLVKTISKSGIKGLYGFVS 180
```

```
OY 181 VGGIIYRAAYFGVYDPAKGMPLDPKNTHIYVSNMIAQTVAVAGVSPPTVARRMM 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VGGIIYRAAYFGVYDPAKGMPLDPKNTHIYVSNMIAQTVAVAGVSPPTVARRMM 240
```

```
OY 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFFKGAWSNVLKMGAFVLVYDELKVI 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYSGITDCKRKIAKDEGSAFFKGAWSNVLKMGAFVLVYDELKVI 298
```

## RESULT 6

O98BV9 PRELIMINARY; PRT; 298 AA.  
AC O98BV9;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Solute carrier family 25.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
DR EMBL; AK078077; BAC37117.1; -;  
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 91.6%; Score 1414; DB 11; Length 298;  
Best Local Similarity 88.6%; Pred. No. 6.8e-120;  
Matches 264; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

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OY 1 MTEQAIISAKDPLAGGIAAISTKAVAPIERVKLLQVQHASKOIAADKOYGVDCIVR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRKLSFLDKPLAGGIAAASKTAVAPIERVKLLQVQHASKOISAKOYGIIDCVRR 60

OY 61 IPKEQGVLSFMRGNLANIYIRYPTQALNPAFKDKTKQIFLGVDKHTQFWRYPAGNLASG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEGGLISFMRGNLANIYIRYPTQALNPAFKDKTKQIFLGVDKHTQFWRYPAGNLASG 120

OY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVKTISDGINLQYGFVS 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSSQREPRGLDCLTKIFKSDGLRGLYGFVS 180

OY 181 VGGIIYRAAYFGVYDPAKGMPLDPKNTHIYVSNMIAQTVAVAGVSPPTVARRMM 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VGGIIYRAAYFGVYDPAKGMPLDPKNTHIYVSNMIAQTVAVAGVSPPTVARRMM 240

OY 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFFKGAWSNVLKMGAFVLVYDELKVI 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGVDCKRKIAKDEGANAFFKGAWSNVLKMGAFVLVYDELKVI 298
```

## RESULT 7

O9PRH1 PRELIMINARY; PRT; 298 AA.  
AC O9PRH1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE ADP/ATP translocase.  
OS Rana rugosa (Wrinkled frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

```

CX NCB1_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -
DR EMBL; AB008456; BAA36506.1; -
DR EMBL; AB008461; BAA36511.1; -
DR EMBL; AB008462; BAA36512.1; -
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mlt carrier.
DR InterPro; IPR002030; Mlt uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ
SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 91.3%; Score 1409; DB 13; Length 298;
Best Local Similarity 88.6%; Pred. No. 1.9e-119;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

CY 1 MTEOASFAKDFLAGGIAAISTKTAVAPIEVRKLLQVQHASKQIADKQYGVDCIVR 60
DB 1 MTDALISFAKDFLAGGVAIAISTKTAVAPIEVRKLLQVQHASKQITADKQYGVDCIVR 60
CY 61 IPKGGVLSFWRGNLANIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSG 120
DB 61 IPKGGVLSFWRGNLANIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSG 120
CY 121 GAAGATSLCFYPPDPAFTRLAADVKGSGTEREFGDGLVKTISDGLYQGFVS 180
DB 121 GAAGATSLCFYPPDPAFTRLAADVKGSGTEREFGDGLVKTISDGLYQGFVS 180
CY 181 VGGIIYRAAYFGYVDKAGMLPDPKNTHTIVSWMIAGTVTAAGVSYPPDVTARRMM 240
DB 181 VGGIIYRAAYFGYVDKAGMLPDPKNTHTIVSWMIAGTVTAAGVSYPPDVTARRMM 240
CY 241 QSGRKGADIMTGVDCWKRIFRDEGGAFFKGAWSNVLKMGAFVLVYDELKCYI 298
DB 241 QSGRKGADIMTGVDCWKRIFRDEGGAFFKGAWSNVLKMGAFVLVYDELKCYI 298

RESULT 8
ID Q9PRH2 PRELIMINARY; PRT; 298 AA.
AC Q9PRH2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
CX NCB1_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008460; BAA36510.1; -
DR EMBL; AB008458; BAA36508.1; -
DR EMBL; AB008459; BAA36509.1; -

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DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mlt carrier.
DR InterPro; IPR002030; Mlt uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ
SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 91.1%; Score 1406; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 3.6e-119;
Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

CY 1 MTEOASFAKDFLAGGIAAISTKTAVAPIEVRKLLQVQHASKQIADKQYGVDCIVR 60
DB 1 MTDALISFAKDFLAGGVAIAISTKTAVAPIEVRKLLQVQHASKQITADKQYGVDCIVR 60
CY 61 IPKGGVLSFWRGNLANIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSG 120
DB 61 IPKGGVLSFWRGNLANIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSG 120
CY 121 GAAGATSLCFYPPDPAFTRLAADVKGSGTEREFGDGLVKTISDGLYQGFVS 180
DB 121 GAAGATSLCFYPPDPAFTRLAADVKGSGTEREFGDGLVKTISDGLYQGFVS 180
CY 181 VGGIIYRAAYFGYVDKAGMLPDPKNTHTIVSWMIAGTVTAAGVSYPPDVTARRMM 240
DB 181 VGGIIYRAAYFGYVDKAGMLPDPKNTHTIVSWMIAGTVTAAGVSYPPDVTARRMM 240
CY 241 QSGRKGADIMTGVDCWKRIFRDEGGAFFKGAWSNVLKMGAFVLVYDELKCYI 298
DB 241 QSGRKGADIMTGVDCWKRIFRDEGGAFFKGAWSNVLKMGAFVLVYDELKCYI 298

RESULT 9
ID Q9YIC4 PRELIMINARY; PRT; 298 AA.
AC Q9YIC4;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
CX NCB1_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008457; BAA36507.1; -
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mlt carrier.
DR InterPro; IPR002030; Mlt uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ
SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
Best Local Similarity 87.9%; Pred. No. 8.3e-119;
Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

CY 1 MTEOASFAKDFLAGGIAAISTKTAVAPIEVRKLLQVQHASKQIADKQYGVDCIVR 60
DB 1 MTDALISFAKDFLAGGVAIAISTKTAVAPIEVRKLLQVQHASKQITADKQYGVDCIVR 60

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Db 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKIMDCVVR 60  
 Qy 1PKEQGVLSFMRGNLANVIRYPTQALNPAFKDKTKOIFLGVDHGTQFMRYFAGNLASG 120  
 Db 61 IPKEQGVLSFMRGNLANVIRYPTQALNPAFKDKTKOIFLNDVDRKTFMRIFAGNLASG 120  
 Qy 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVKITKSDIRGLYQGSFVS 180  
 Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVKITKSDIRGLYQGSFVS 180  
 Qy 181 VOGIIITRAAFVGYDTAKGMLPDPKNTHTIVSMIAQSVTAAGFASYPEDTVRRMM 240  
 Db 181 VOGIIITRAAFVGYDTAKGMLPDPKNTHTIVSMIAQSVTAAGFASYPEDTVRRMM 240  
 Qy 241 OSGRKADIMYTGVDWCARKIFRDEGKAFKFGKANSVLRGKGFVLVDELKCVI 298  
 Db 241 OSGRKADIMYTGVDWCARKIFRDEGKAFKFGKANSVLRGKGFVLVDELKCVI 298

## RESULT 10

Q95VX4 PRELIMINARY; PRT; 299 AA.  
 AC Q95VX4;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE ADP-ATP translocase.  
 OS Ethmostigmus rubripes.  
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;  
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.  
 OX NCBI\_TaxId=62613;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Butnell J.N.;  
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus  
 rubripes";  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
 RL EMBL; AF401758; AAL02100.1; -;  
 DR InterPro; IPR001993; Mitochondrion.  
 DR InterPro; IPR002067; Mito\_cariier.  
 DR Pfam; PF00153; mito\_cariier.  
 DR PRINTS; PR00926; MITOCARIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 SQ SEQUENCE 299 AA; 33037 MW; 3C3BGB26E7C3C5E CRC64;

Query Match 84.3%; Score 1300; DB 5; Length 299;  
 Best Local Similarity 81.5%; Pred. No. 1.5e-109;  
 Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKIMDCVVR 60  
 Db 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKIMDCVVR 60  
 Qy 61 IPKEQGVLSFMRGNLANVIRYPTQALNPAFKDKTKOIFLGVDHGTQFMRYFAGNLASG 120  
 Db 61 IPKEQGVLSFMRGNLANVIRYPTQALNPAFKDKTKOIFLNDVDRKTFMRIFAGNLASG 120  
 Qy 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVKITKSDIRGLYQGSFVS 180  
 Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVKITKSDIRGLYQGSFVS 180  
 Qy 181 VOGIIITRAAFVGYDTAKGMLPDPKNTHTIVSMIAQSVTAAGFASYPEDTVRRMM 240  
 Db 181 VOGIIITRAAFVGYDTAKGMLPDPKNTHTIVSMIAQSVTAAGFASYPEDTVRRMM 240  
 Qy 241 OSGRKADIMYTGVDWCARKIFRDEGKAFKFGKANSVLRGKGFVLVDELKCVI 298  
 Db 241 OSGRKADIMYTGVDWCARKIFRDEGKAFKFGKANSVLRGKGFVLVDELKCVI 298

RESULT 11  
 Q91336 PRELIMINARY; PRT; 317 AA.

AC Q91336;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS Rana sylvatica (Wood frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
 OX NCBI\_TaxId=45438;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Liver;  
 RC MEDLINE=97398141; PubMed=9256066;  
 RA Cai Q., Greenway S.C., Storey K.B.;  
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene  
 in wood frog under freezing stress";  
 RL Biochim. Biophys. Acta 1353:69-78 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cai Q., Storey K.B.;  
 RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; U44832; AAA97882.2; -;  
 DR InterPro; IPR001993; Mitochondrion.  
 DR InterPro; IPR002067; Mito\_cariier.  
 DR Pfam; PF00153; mito\_cariier.  
 DR PRINTS; PR00926; MITOCARIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 317 AA; 35005 MW; 5F66B7BD8D5CEB72 CRC64;

Query Match 81.6%; Score 1259; DB 13; Length 317;  
 Best Local Similarity 86.8%; Pred. No. 8.2e-106;  
 Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKIMDCVVR 60  
 Db 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKIMDCVVR 60  
 Qy 61 IPKEQGVLSFMRGNLANVIRYPTQALNPAFKDKTKOIFLGVDHGTQFMRYFAGNLASG 120  
 Db 61 IPKEQGVLSFMRGNLANVIRYPTQALNPAFKDKTKOIFLNDVDRKTFMRIFAGNLASG 120  
 Qy 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVKITKSDIRGLYQGSFVS 180  
 Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVKITKSDIRGLYQGSFVS 180  
 Qy 181 VOGIIITRAAFVGYDTAKGMLPDPKNTHTIVSMIAQSVTAAGFASYPEDTVRRMM 240  
 Db 181 VOGIIITRAAFVGYDTAKGMLPDPKNTHTIVSMIAQSVTAAGFASYPEDTVRRMM 240  
 Qy 241 OSGRKADIMYTGVDWCARKIFRDEGKAFKFGKANSVLRGKGFVLVDELKCVI 298  
 Db 241 OSGRKADIMYTGVDWCARKIFRDEGKAFKFGKANSVLRGKGFVLVDELKCVI 298

RESULT 12  
 Q81RAO PRELIMINARY; PRT; 312 AA.  
 AC Q81RAO;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE CG16944-PC.  
 GN SEB.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George S.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benson P.V., Bhandari D., Binkley S.,  
 RA Borkov D., Botchan M.R., Bouck J., Brocktein P., Brotter P.,  
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,  
 RA Fodor C., Gong F., Gorrell J.H., Gu Z., Guan P., Harlie M.,  
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harlie M.,  
 RA Harris N.L., Harvey D., Helman J.D., Hernandez J.R., Houck J.,  
 RA Hosteln D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.R., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laevo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Metkulov G., Milshina N.V., Modary C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodgett M., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhu X., Zhu S., Zhu L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*.";  
 RA Science 287:2185-2195 (2000).  
 RA [2]  
 RA SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorssett V., Doup L.E., Doyle C., Dreenek D., Parfan D.,  
 RA Ferriere S., Fries E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hosteln D., Howland T.J.,  
 RA Idegawa C., Jaitani M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacle J.M., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phoonanavong S., Peltman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RA "Sequencing of *Drosophila melanogaster* genome.";  
 RA Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.  
 RA [3]  
 RA SEQUENCE FROM N.A.  
 RA Miya S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Bernan B., Carlson J.W., Celniker S.E.,  
 RA Clump M., Drysdale R., Emmert D., Fries B., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,  
 RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield B.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RA "Annotation of *Drosophila melanogaster* genome.";  
 RA Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.  
 RA [4]  
 RA SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;  
 RA Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.  
 RA [5]  
 RA SEQUENCE FROM N.A.

RA FlyBase;  
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RA EMBL; AB003484; AAN09267.1;  
 RA SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;  
 RA Query Match 81.3%; Score 1254.5; DB 5; Length 312;  
 RA Best Local Similarity 80.6%; Pred. No. 2.1e-105;  
 RA Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;  
 QY 5 AIFAKDPLAGIAAIAISKTVAPIERVKLLQVQHASKOIAADKOYKGIYDCIIRPKE 64  
 DB 20 AVGFVKDPAAGISAAVSKTAVAPIERVKLLQVQHSIKQISPDQKGMVDCFIIRPKE 79  
 QY 65 QGVLSFWNGNLAVIRYPTQALNFAFQKTKQIFLGVVDKHTQFWRYPAGNLASGGAAG 124  
 DB 80 QGFPSFWNGNLAVIRYPTQALNFAFQKTKQIFLGVVDKHTQFWRYPAGNLASGGAAG 139  
 QY 125 ATSLCFVYPLDPARTLADYVGSSTREPGILGCLVKITKSDGIRGLQGSFVSVOGI 184  
 DB 140 ATSLCFVYPLDPARTLADYVGSSTREPGILGCLVKITKSDGIRGLQGSFVSVOGI 198  
 QY 185 IYRAAYFVDYAKGMLPDEKNTIIVSWIAQTVAAGVSYFPDTRRRMMQSGR 244  
 DB 199 IYRAAYFVDYAKGMLPDEKNTIIVSWIAQTVAAGVSYFPDTRRRMMQSGR 258  
 QY 245 KGADIMYTGVDQWKEIRFDGKGAFFGKANSVIRGKGAFAVLYBELKVI 298  
 DB 259 KATEVIYKNTLHCWATIKQGTGAFKGAFAVLYBELKVI 312  
 RESULT 13  
 QY Q9NHM5 PRELIMINARY; PRT; 300 AA.  
 AC Q9NHM5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DB ADP/ATP translocase.  
 OS *Lucilia cuprina* (Greenbottle fly) (Australian sheep blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; *Lucilia*.  
 OK NCBI\_Taxid=7375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SS mal seeking;  
 RA "A CDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 CC EMBL; AF218587; AAF32322.1;  
 DR InterPro: IPR001993; Mitoch carrier.  
 DR InterPro: IPR002067; Mitoch carrier.  
 DR Pfam: PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER, 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EAD2E742 CRC64;  
 QY Query Match 80.1%; Score 1235.5; DB 5; Length 300;  
 QY Best Local Similarity 79.5%; Pred. No. 1e-103;  
 QY Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;  
 DB 9 LGFVDFPAAGISAAVSKTAVAPIERVKLLQVQHSIKQISPDQKGMVDCFIIRPKE 68  
 QY 66 GVLTSFWNGNLAVIRYPTQALNFAFQKTKQIFLGVVDKHTQFWRYPAGNLASGGAAG 125  
 DB 69 GFASTYRWGNANVIRYPTQALNFAFQKTKQIFLGVVDKHTQFWRYPAGNLASGGAAG 128  
 QY 126 TSLCFVYPLDPARTLADYVGSSTREPGILGCLVKITKSDGIRGLQGSFVSVOGI 185



Db 129 TSLCFVYPLDPAFRTLAADTGKG-QREFTGLGNCILAKIPKSGDVGVLKRGFVSGVGGI 187

Qy 166 IYRAAYFGVYDPAKGMPLDPKXTHIVSMIAQVTTAVAGVSYPPDTRRRMMQSGRK 245

Db 188 IYRAAYFGVYDPAKGMPLDPKXTHIVSMIAQVTTAVAGVSYPPDTRRRMMQSGRK 247

Qy 246 GADIMYTGTVDCMRKIFRDEGKAPFKGANSNVLKMGGAFAVLVYDELKXVI 298

Db 248 ATETIYKNTLHCWATIAKQEGTGAFFKAFSNVLKGTGAFVLVYDELKXVI 300

RESULT 14

044093 PRELIMINARY; PRT; 288 AA.

AC 044093;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).

GN SEB.

OS Drosophila pseudobscura (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI\_TaxID=7237;

OX NCBI\_TaxID=7237;

RN [1]

RP SEQUENCE FROM N.A.

RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.,

RL Genetics 0:0-0(1997).

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AF025799; AAB87883.1; -.

DR FLYBASE; FBgn023237; Dros.\seeb.

DR InterPro; IPR001993; Mitoch\_carrier.

DR InterPro; IPR002067; Mit\_carrier.

DR Pfam; PF00153; mito\_carr; 3.

DR PRINTS; PR00926; MITOCARRIER.

DR PROSITE; PS00215; MITOCH CARRIER; 3.

KW Membrane; Repeat; Transmembrane; Transport.

FT NON TER 288

SQ SEQUENCE 288 AA; 31725 MW; 052B0CC050436B0 CRC64;

Query Match 77.0%; Score 1187.5; DB 5; Length 288;

Best Local Similarity 80.7%; Pred. No. 2.2e-99;

Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

Qy 5 AISPADFLAGGIAAISTKTAAPLIERVLLQVGHASKQIADKQYKGIYDCIVRIPE 64

Db 7 AIGFYKDFPAAGISAAVSKTAVAPIERVKLLQVGHISKQISPDKQYKGMVDCFRIPRE 66

Qy 65 QGVLSFMRGNLANVIRYPTQALNPAFDKXKQIFLGVDKHTQWRPFAGNLASGGAAG 124

Db 67 QGFSSFWRGNLANVIRYPTQALNPAFDKXKQIFLGVDKHTQWRPFAGNLASGGAAG 126

Qy 125 ATSLCFVYPLDPAFRTLAADVGKSTEREFGDCLVITKSDGIRGLYOGFSVSGOI 184

Db 127 ATSLCFVYPLDPAFRTLAADVGKQ-QREFTGLGNCILAKIPKSGDVGVLKRGFVSGVGGI 185

Qy 185 IYRAAYFGVYDPAKGMPLDPKXTHIVSMIAQVTTAVAGVSYPPDTRRRMMQSGR 244

Db 186 IYRAAYFGVYDPAKGMPLDPKXTHIVSMIAQVTTAVAGVSYPPDTRRRMMQSGR 244

Qy 245 KGAIDIMYTGTVDCMRKIFRDEGKAPFKGANSNVLKMGGAFAVLV 289

Db 245 KATETIYKNTLHCWATIAKQEGTGAFFKAFSNVLKGTGAFVLV 288

RESULT 15

044094 PRELIMINARY; PRT; 288 AA.

AC 044094;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).

GN SEB.

OS Drosophila subobscura (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7241;

RN [1]

RP SEQUENCE FROM N.A.

RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.,

RL Genetics 0:0-0(1997).

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AF025799; AAB87884.1; -.

DR FLYBASE; FBgn023237; Dros.\seeb.

DR InterPro; IPR001993; Mitoch\_carrier.

DR InterPro; IPR002067; Mit\_carrier.

DR Pfam; PF00153; mito\_carr; 3.

DR PRINTS; PR00926; MITOCARRIER.

DR PROSITE; PS00215; MITOCH CARRIER; 3.

KW Membrane; Repeat; Transmembrane; Transport.

FT NON TER 288

SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;

Best Local Similarity 80.4%; Pred. No. 5e-99;

Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

Qy 5 AISPADFLAGGIAAISTKTAAPLIERVLLQVGHASKQIADKQYKGIYDCIVRIPE 64

Db 7 AMGFYKDFPAAGISAAVSKTAVAPIERVKLLQVGHISKQISPDKQYKGMVDCFRIPRE 66

Qy 65 QGVLSFMRGNLANVIRYPTQALNPAFDKXKQIFLGVDKHTQWRPFAGNLASGGAAG 124

Db 67 QGFSSFWRGNLANVIRYPTQALNPAFDKXKQIFLGVDKHTQWRPFAGNLASGGAAG 126

Qy 125 ATSLCFVYPLDPAFRTLAADVGKSTEREFGDCLVITKSDGIRGLYOGFSVSGOI 184

Db 127 ATSLCFVYPLDPAFRTLAADVGKQ-QREFTGLGNCILAKIPKSGDVGVLKRGFVSGVGGI 185

Qy 185 IYRAAYFGVYDPAKGMPLDPKXTHIVSMIAQVTTAVAGVSYPPDTRRRMMQSGR 244

Db 186 IYRAAYFGVYDPAKGMPLDPKXTHIVSMIAQVTTAVAGVSYPPDTRRRMMQSGR 244

Qy 245 KGAIDIMYTGTVDCMRKIFRDEGKAPFKGANSNVLKMGGAFAVLV 289

Db 245 KATETIYKNTLHCWATIAKQEGTGAFFKAFSNVLKGTGAFVLV 288

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Job time : 31.701 secs

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